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OM protein - protein search, using BW model

Run on: December 24, 2005, 10:35:05 ; Search time 166 Seconds
(without alignments)
415.756 Million cell updates/sec

Title: US-10-789-129-2
Perfect score: 910
Sequence: 1 MKASSLAFSLSAFYLLWT.....AVVKALGELDILLQWMEETE 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Liciting first 45 summaries

Database :

A_Geneseq_21:.*
1: geneseqp1980s:.*
2: geneseqp1980s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 910 | 100.0 | 176 | 2 | AAy08661 Human Zcy |
| 2 | 910 | 100.0 | 176 | 4 | AA855259 Human int |
| 3 | 910 | 100.0 | 176 | 4 | AAU04049 Human int |
| 4 | 910 | 100.0 | 176 | 5 | ABG67190 Inflamat |
| 5 | 910 | 100.0 | 176 | 5 | AAE29052 Human IL- |
| 6 | 910 | 100.0 | 176 | 6 | ABR62464 Human int |
| 7 | 910 | 100.0 | 176 | 7 | ABW00889 Human Zcy |
| 8 | 910 | 100.0 | 176 | 7 | ADG46669 Human Zcy |
| 9 | 910 | 100.0 | 176 | 8 | ADJ83281 Human int |
| 10 | 910 | 100.0 | 176 | 8 | ADM95041 Human int |
| 11 | 910 | 100.0 | 176 | 8 | ADQ88067 Human Zcy |
| 12 | 910 | 100.0 | 176 | 8 | ADR16328 Human Zcy |
| 13 | 910 | 100.0 | 176 | 8 | ADSI8363 Human Zcy |
| 14 | 910 | 100.0 | 176 | 9 | ADV66904 Human IL- |
| 15 | 910 | 100.0 | 176 | 9 | ADW64518 Human IL- |
| 16 | 910 | 100.0 | 176 | 9 | ADX58772 Interleuk |
| 17 | 910 | 100.0 | 176 | 9 | AEA50049 Full leng |
| 18 | 910 | 100.0 | 176 | 9 | AEA28787 Human int |
| 19 | 906 | 99.6 | 176 | 4 | AAU12220 Human PRO |
| 20 | 906 | 99.6 | 176 | 5 | ABP52427 Human LP8 |
| 21 | 906 | 99.6 | 176 | 5 | AB882287 Human LP8 |
| 22 | 906 | 99.6 | 176 | 6 | AB017664 Novel hum |
| 23 | 906 | 99.6 | 176 | 6 | ABU80918 Human PRO |
| 24 | 906 | 99.6 | 176 | 6 | ABU66618 Human PRO |

| | | | | | |
|----|-----|------|-----|---|--------------------|
| 25 | 906 | 99.6 | 176 | 6 | ABU59699 Novel sec |
| 26 | 906 | 99.6 | 176 | 6 | ABO24889 Human sec |
| 27 | 906 | 99.6 | 176 | 6 | ABU66894 Human sec |
| 28 | 906 | 99.6 | 176 | 6 | ADA45617 Novel hum |
| 29 | 906 | 99.6 | 176 | 6 | ADA76048 Human PRO |
| 30 | 906 | 99.6 | 176 | 6 | ADA18698 Human PRO |
| 31 | 906 | 99.6 | 176 | 6 | ADA61321 Homo sapl |
| 32 | 906 | 99.6 | 176 | 6 | ADA19106 Novel hum |
| 33 | 906 | 99.6 | 176 | 6 | ADA27647 Human PRO |
| 34 | 906 | 99.6 | 176 | 6 | ADA86126 Novel hum |
| 35 | 906 | 99.6 | 176 | 6 | ADA15690 Human PRO |
| 36 | 906 | 99.6 | 176 | 6 | ADA47476 Human PRO |
| 37 | 906 | 99.6 | 176 | 6 | ADA67271 Human PRO |
| 38 | 906 | 99.6 | 176 | 6 | ADA30278 Human PRO |
| 39 | 906 | 99.6 | 176 | 6 | ADA85574 Novel hum |
| 40 | 906 | 99.6 | 176 | 6 | ADA96786 Human PRO |
| 41 | 906 | 99.6 | 176 | 6 | ADA79090 Human PRO |
| 42 | 906 | 99.6 | 176 | 6 | ADA87229 Novel hum |
| 43 | 906 | 99.6 | 176 | 6 | ADA16431 Human PRO |
| 44 | 906 | 99.6 | 176 | 6 | ADA91523 Novel hum |
| 45 | 906 | 99.6 | 176 | 6 | ADA14586 Human PRO |

ALIGNMENTS

RESULT 1
ID AAY08661 standard; protein; 176 AA.
XX
AC AAY08661;
XX
DT 09-AUG-1999 (first entry)
XX
DE Human Zcyto10 allele 1 protein.
XX
KW Zcyto10; four alpha helix cytokine; vulnery; cyrostatic; haemostatic;
KW anti-inflammatory; anti-asthmatic; growth factor; maintenance factor;
KW trachea; salivary gland; stomach; pancreas; muscle; gene therapy; cancer;
KW proliferation; differentiation; modulator; gastrointestinal tract;
KW oral cavity; asthma; tracheobronchial tract; bronchitis; wound healing;
KW platelet count; thrombocytopenia; human.
XX
OS Homo sapiens.
XX
XX WO9927103-A1.
XX
PD 03-JUN-1999.
XX
PF 25-NOV-1998; 98MO-US025228.
XX
PR 26-NOV-1997; 97US-00979156.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Conklin DC, Haldeman BA, Grossmann A;
XX
XX WPI; 1999-357840/30.
XX
DR N-PSDB; AAX77692.
XX
PT New mammalian cytokine-like polynucleotide useful in the treatment of
XX
XX Claim 1; Page 64-65; 82pp; English.
XX
PS This invention describes a novel mammalian four alpha helix cytokine
XX designated Zcyto10 which has vulnery, cyrostatic, anti-inflammatory,
XX anti-asthmatic and haemostatic activity. Zcyto10 may be a growth and/or
XX maintenance factor in the trachea and salivary glands, stomach, pancreas
XX and muscle. Zcyto10 polynucleotides are useful as sources of primers and
XX probes, and to determine if the Zcyto10 gene is present on chromosome 1,
XX or to detect any mutations that may have occurred. Zcyto10
XX polynucleotides are also useful as gene therapy reagents. The Zcyto10

CC polypeptide, its fragments, and antibodies, as well as compounds
CC identified as having binding affinity to Zcyto10, should be useful in the
CC treatment of conditions associated with abnormal physiology or
CC development, including abnormal proliferation, e.g. cancerous conditions,
CC or degenerative conditions or altered immunity. The products are also
CC useful for modulating cell proliferation, cell differentiation or
CC cytokine production in the prevention or treatment of conditions
CC characterized by abnormal cell proliferation, cell differentiation or
CC cytokine production. Zcyto10 polypeptides, agonists and antagonists may
CC be therapeutically useful in the regeneration of the gastrointestinal
CC tract or oral cavity, as well as in the treatment of asthma, and other
CC diseases of the tracheobronchial tract such as bronchitis. Zcyto10
CC polypeptides may also be useful to promote wound healing, and to increase
CC platelet count, e.g. in cancer patients who experience thrombocytopenia
CC due to chemotherapy or radiation therapy

SQ Sequence 176 AA;

Query Match 100.0%; Score 910; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLAFSLISAFFYLLMTPTSGTKLTNLGSCVIATNLQEIRNGFSDIRGSVQAKDGN 60
DB 1 MKASSLAFSLISAFFYLLMTPTSGTKLTNLGSCVIATNLQEIRNGFSDIRGSVQAKDGN 60
QY 61 DIRILRTESLQDTKPNRCCCLRHLLRLYLDRVFKNYQTPDHYTLRKISSLSANSLTLTK 120
DB 61 DIRILRTESLQDTKPNRCCCLRHLLRLYLDRVFKNYQTPDHYTLRKISSLSANSLTLTK 120
QY 121 KDRLCHAHMTCHGGEAMKKYSQILSHPEKLEPQAAVVKALGELDILQMEETE 176
DB 121 KDRLCHAHMTCHGGEAMKKYSQILSHPEKLEPQAAVVKALGELDILQMEETE 176

RESULT 2

AAB85259 standard; protein; 176 AA.

AC AAB85259;

DT 07-SEP-2001 (first entry)

DE Human interleukin-20 (IL-20) receptor polypeptide.

KW Interleukin 20; IL-20; IL-20RA; ZcytoR7; IL-20RB; DIRS1; immunoglobulin;

KM antiinflammatory; antipsoriatic; antiaesthetic; antibacterial;

KW dermatological; antitumor; antagonist.

OS Homo sapiens.

PN WO200146232-A2.

PD 28-JUN-2001.

PF 22-DEC-2000; 2000WO-US035307.

PR 23-DEC-1999; 99US-00471774.

PR 22-JUN-2000; 2000US-0213416P.

PA (ZYMO) ZYMOGENETICS INC.

PI Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;

PI Rixon MW, Presnell SR, Fox BA;

PI WPI; 2001-398320/42.

PT Isolated interleukin 20 soluble receptor comprising two polypeptide

PT subunits IL-20RA and IL-20RB, useful for down-regulating IL-20 and thus

PT treating inflammatory diseases such as psoriasis.

PS Disclosure; Page 53-54; 119pp; English.

CC The invention relates to an interleukin 20 (IL-20) soluble receptor
CC comprising two polypeptide subunits IL-20RA (formerly known as ZcytoR7)
CC and IL-20RB (formerly known as DIRS1). The two subunits are preferably
CC linked together. In one embodiment, one subunit is fused to the constant
CC region of the light chain of an immunoglobulin, and the other subunit is
CC fused to constant region of the heavy chain of an immunoglobulin. The
CC light chain and the heavy chain are connected via a disulphide bond. The
CC soluble receptor can be used to down-regulate IL-20 and thus treat
CC inflammatory diseases such as psoriasis, inflammatory lung injury such as
CC asthma or bronchitis, adult respiratory disease (ARD), septic shock,
CC multiple organ failure, bacterial pneumonia, eczema, atopic and contact
CC dermatitis, and inflammatory bowel disease such as ulcerative colitis and
CC Crohn's disease. Sequences AAB85259-262 represent human IL-20 receptor
CC polypeptide fragments

SQ Sequence 176 AA;

Query Match 100.0%; Score 910; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLAFSLISAFFYLLMTPTSGTKLTNLGSCVIATNLQEIRNGFSDIRGSVQAKDGN 60
DB 1 MKASSLAFSLISAFFYLLMTPTSGTKLTNLGSCVIATNLQEIRNGFSDIRGSVQAKDGN 60
QY 61 DIRILRTESLQDTKPNRCCCLRHLLRLYLDRVFKNYQTPDHYTLRKISSLSANSLTLTK 120
DB 61 DIRILRTESLQDTKPNRCCCLRHLLRLYLDRVFKNYQTPDHYTLRKISSLSANSLTLTK 120
QY 121 KDRLCHAHMTCHGGEAMKKYSQILSHPEKLEPQAAVVKALGELDILQMEETE 176
DB 121 KDRLCHAHMTCHGGEAMKKYSQILSHPEKLEPQAAVVKALGELDILQMEETE 176

RESULT 3

AAU04049 standard; protein; 176 AA.

AC AAU04049;

DT 23-OCT-2001 (first entry)

DE Human interleukin-20, IL-20, protein #1.

KW Human; interleukin-20; IL-20; antagonist; psoriasis; eczema; dermatitis;

KW adult respiratory disease; asthma; bronchitis; pneumonia;

KW multiple organ failure; inflammatory lung injury; septic shock;

KW bacterial pneumonia; inflammatory bowel disease; rheumatoid arthritis;

KW ulcerative colitis; Crohn's disease.

OS Homo sapiens.

PN WO200146261-A1.

PD 28-JUN-2001.

PF 22-DEC-2000; 2000WO-US035305.

PR 23-DEC-1999; 99US-00470898.

PR 22-JUN-2000; 2000US-0213416P.

PA (ZYMO) ZYMOGENETICS INC.

PI Thompson P, Foster DC, Wenfeng X, Madden KL, Kelly JD;

PI Sprecher CA, Blumberg H, Sagan MA, Jaspers SR, Chandrasekhar JA;

PI Novak JE;

PI WPI; 2001-418045/44.

PT Treating interleukin-20 induced inflammation in a mammal, such as adult

PT respiratory disease, eczema, psoriasis, contact dermatitis, multiple

PT organ failure and septic shock, involves administering IL-20 antagonist.

PS Claim 1; Page 47-48; 117pp; English.

XX The sequence is a Human interleukin-20, IL-20 protein of the invention.

CC The invention relates to treating a mammal afflicted with a disease in

CC which an interleukin-20 (IL-20) polypeptide plays a role, involves

CC administering antagonist of IL-20 polypeptide to the individual. The

CC method is useful for treating psoriasis, eczema, atopic dermatitis,

CC contact dermatitis, adult respiratory disease, asthma, bronchitis and

CC pneumonia and is also useful for treating multiple organ failure,

CC inflammatory lung injury, septic shock, bacterial pneumonia, inflammatory

CC bowel disease, rheumatoid arthritis, ulcerative colitis and Crohn's

CC disease

XX

SQ Sequence 176 AA;

Query Match 100.0%; Score 910; DB 4; Length 176;

Best Local Similarity 100.0%; Pred. No. 5e-88;

Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLAFLSAAFYLLMTPTSTGLKTNLNGSCVIATNLQEIIRNGFSIDIRGVSQAKDGN1 60

DB 1 MKASSLAFLSAAFYLLMTPTSTGLKTNLNGSCVIATNLQEIIRNGFSIDIRGVSQAKDGN1 60

QY 61 DIRILRTESLQDTKPRANRCCLLRHLLRLYLDRVFNKYQTPDHYTLRKISSLANSEFLTK 120

DB 61 DIRILRTESLQDTKPRANRCCLLRHLLRLYLDRVFNKYQTPDHYTLRKISSLANSEFLTK 120

QY 121 KDRLCHAHMTCHGCEBAMKCKYSQILSHPEKLEPOAAVVKALGELDILLQWMEETE 176

DB 121 KDRLCHAHMTCHGCEBAMKCKYSQILSHPEKLEPOAAVVKALGELDILLQWMEETE 176

RESULT 4

ABG67190

ID ABG67190 standard; protein; 176 AA.

XX

AC ABG67190;

XX

DT 24-SEP-2002 (first entry)

XX

DE Inflammatory disease related human interleukin (IL) 20 polypeptide #1.

XX

KW Inflammation; interleukin-20; IL-20; interleukin-8; IL-8; chemokine;

KW neutrophil; monocyte; basophil; eosinophil; chemotactant; psoriasis;

KW periodontal disease; rheumatoid arthritis; idiopathic pulmonary fibrosis;

KW angiogenesis-dependent chronic inflammatory condition; lung cancer;

KW melanoma; inflammatory disease; diabetes; arteriosclerosis; cataract;

KW reperfusion injury; cancer; meningitis; rheumatic disease; skin disease;

KW idiopathic pulmonary fibrosis; inflammatory bowel disease; psoriasis;

KW ulcerative colitis; eczema; atopic dermatitis; contact dermatitis;

KW inflammatory lung disease; ARD; adult respiratory disease; asthma;

KW bronchitis; pneumonia.

XX

OS Homo sapiens.

XX

PN US2002042366-A1.

XX

PD 11-APR-2002.

XX

PF 22-DEC-2000; 2000US-00746359.

XX

PR 23-DEC-1999; 99US-0171969P.

PR 22-JUN-2000; 2000US-0213341P.

XX

PA (THOM/) THOMPSON P.

PA (FOST/) FOSTER D C.

PA (XUWU/) XU W.

PA (MADD/) MADDEN K L.

PA (KELL/) KELLY J D.

PA (SPRE/) SPRECHER C A.

PA (BLUM/) BLUMBERG H.

PA (EAGAN/) EAGAN M A.

PA (JASPER/) JASPERS S R.

PA (CHAN/) CHANDRASEKHAR Y A.

PA (NOVA/) NOVAK J E.

XX

PI Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA;

PI Blumberg H, Eagan MA, Jaspers SR, Chandrasekhar YA, Novak JE;

XX

DR WPI; 2002-507215/54.

XX

PT Treating inflammatory skin and lung diseases using antibodies against

PT interleukins (IL)-20 (which indirectly modulates activation of IL-8),

PT useful for treating e.g. psoriasis, asthma and bronchitis.

XX

PS Claim 1; Page 12-13; 68pp; English.

XX

CC The invention describes a method (I) for treating a mammal afflicted with

CC a disease in which an interleukin-20 (IL-20) polypeptide plays a role

CC comprising administering antagonist of the IL-20 polypeptide to the

CC individual. An important cytokine in the inflammatory process is

CC interleukin-8 (IL-8), a chemokine that acts as an agonist for neutrophils

CC via chemotaxis and the release of granule enzymes. IL-8 binds to

CC receptors on neutrophils, monocytes, basophils, and eosinophils. IL-8 is

CC a potent chemottractant for neutrophils; and the early stages of

CC periodontal disease are characterized by the influx of neutrophils. IL-8

CC is a potent inducer of angiogenesis in several angiogenesis-dependent

CC chronic inflammatory conditions, including rheumatoid arthritis,

CC psoriasis, and idiopathic pulmonary fibrosis. Additionally, IL-8 is an

CC important source of angiogenic activity in human lung cancer. Also, IL-8

CC expression correlates with experimental metastatic activity of some

CC melanoma cell lines. Therefore an effective method to treat inflammatory

CC diseases would be to administer an agent that would inhibit IL-8. It has

CC been shown that IL-20 up-regulates IL-8. Therefore antagonists to IL-20

CC can be used to treat these diseases. The method is used for treating

CC diseases in which the IL-20 polypeptide plays a role e.g. inflammatory

CC diseases including diabetes, arteriosclerosis, cataracts, reperfusion

CC injury, cancer, meningitis, rheumatic diseases, idiopathic pulmonary

CC fibrosis, inflammatory bowel disease (ulcerative colitis), skin disease

CC (psoriasis, eczema, atopic dermatitis and contact dermatitis) or an

CC inflammatory lung disease (adult respiratory disease (ARD), asthma,

CC bronchitis and pneumonia). This sequence represents a human interleukin-

CC 20 (IL-20) polypeptide used in developing the method of the invention

XX

SQ Sequence 176 AA;

Query Match 100.0%; Score 910; DB 5; Length 176;

Best Local Similarity 100.0%; Pred. No. 5e-88;

Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLAFLSAAFYLLMTPTSTGLKTNLNGSCVIATNLQEIIRNGFSIDIRGVSQAKDGN1 60

DB 1 MKASSLAFLSAAFYLLMTPTSTGLKTNLNGSCVIATNLQEIIRNGFSIDIRGVSQAKDGN1 60

QY 61 DIRILRTESLQDTKPRANRCCLLRHLLRLYLDRVFNKYQTPDHYTLRKISSLANSEFLTK 120

DB 61 DIRILRTESLQDTKPRANRCCLLRHLLRLYLDRVFNKYQTPDHYTLRKISSLANSEFLTK 120

QY 121 KDRLCHAHMTCHGCEBAMKCKYSQILSHPEKLEPOAAVVKALGELDILLQWMEETE 176

DB 121 KDRLCHAHMTCHGCEBAMKCKYSQILSHPEKLEPOAAVVKALGELDILLQWMEETE 176

RESULT 5

AAE29052

ID AAE29052 standard; protein; 176 AA.

XX

AC AAE29052;

XX

DT 27-JAN-2003 (first entry)

XX

DE Human IL-20 protein #1.

XX

KW Human; heterodimeric cytokine receptor; interleukin-22R; IL-22R; asthma;

KW inflammatory disease; psoriasis; adult respiratory disease; bronchitis;

KW septic shock; multiple organ failure; inflammatory lung injury; eczema;

KW bacterial pneumonia; dermatitis; ulcerative colitis; Crohn's disease;
 KW antiinflammatory; dermatological; antibacterial; immunosuppressive;
 KW antitumor; ZcytoR11.
 OS Homo sapiens.
 XX
 XX MO200272607-A2.
 XX
 XX 19-SEP-2002.
 XX
 XX 07-MAR-2002; 2002MO-US007214.
 XX
 XX 09-MAR-2001; 2001US-0274560P.
 XX 21-JUN-2001; 2001US-0299865P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Chandrasekher YA, Novak JE, Foster DC, Xu W, Jaspers SR;
 PI WPI; 2002-723314/78.
 XX
 XX Soluble heterodimeric cytokine receptor useful for down-regulating
 PT interleukin-20 and treating inflammatory diseases, such as psoriasis and
 PT asthma, comprises an interleukin-22R subunit and a interleukin-20R8
 PT subunit.
 XX
 XX Disclosure; Page 48; 82pp; English.
 XX
 XX The present invention relates to novel heterodimeric cytokine receptor
 CC which comprises an interleukin-22R (IL-22R; ZcytoR11) subunit. Receptor
 CC sequences are useful for down-regulating IL-20 and treating inflammatory
 CC diseases such as psoriasis, adult respiratory disease, multiple organ
 CC failure, septic shock, inflammatory lung injury such as bronchitis or
 CC asthma, bacterial pneumonia, eczema, atopic and contact dermatitis,
 CC ulcerative colitis and Crohn's disease. The present sequence is human
 CC interleukin-20 (IL-20) protein
 CC
 XX
 SQ Sequence 176 AA;
 Query Match 100.0%; Score 910; DB 5; Length 176;
 Best Local Similarity 100.0%; Pred. No. 5e-88;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKASSLAFSLISAFFYLMTPTGTLNMGSCVIATNLQEIIRNGFSDIRGSVOAKDGI 60
 DB 1 MKASSLAFSLISAFFYLMTPTGTLNMGSCVIATNLQEIIRNGFSDIRGSVOAKDGI 60
 QY 61 DIRILRRTESTLODTKPNRCCILRLRLYLDRVFKNVOTPPHYTLRKISLSANSFLTK 120
 DB 61 DIRILRRTESTLODTKPNRCCILRLRLYLDRVFKNVOTPPHYTLRKISLSANSFLTK 120
 QY 121 KDRLCHAHMTCHGSEAMKKYSQILSHFEKLEPQAAVVKAAGELDIILQMEETE 176
 DB 121 KDRLCHAHMTCHGSEAMKKYSQILSHFEKLEPQAAVVKAAGELDIILQMEETE 176
 RESULT 6
 ID ABR62464 standard; protein; 176 AA.
 XX
 AC ABR62464;
 XX
 XX 06-NOV-2003 (first entry)
 XX
 DE Human interleukin-20.
 XX
 KW Human; interleukin-20; IL-20; cervical cancer; cytostatic; virucide.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..24
 FT Peptide /label= Signal_peptide

FT Protein 25..176
 FT /label= IL-20
 XX
 XX MO2003051384-A1.
 XX
 XX 26-JUN-2003.
 XX
 XX 17-DEC-2002; 2002MO-US040309.
 XX
 XX 17-DEC-2001; 2001US-0341783P.
 XX
 XX (LUNN/) LUNN P G.
 XX
 XX Chandrasekher YA, McKernan PA;
 PI WPI; 2003-569114/53.
 XX
 XX N-PSDB; ACF05161.
 DR
 XX
 XX Inhibiting the growth and/or proliferation of cervical cancer cells,
 PT useful for treating cervical cancer or human papilloma virus infection,
 PT comprises bringing Interleukin-20 (IL-20) into contact with the cervical
 PT cancer cells.
 XX
 XX Disclosure; Page 12; 26pp; English.
 XX
 XX The present sequence is the protein sequence of human interleukin-20 (IL-
 CC 20), including the signal sequence. The invention relates to the use of
 CC IL-20 for treating cervical cancer or cells infected with human papilloma
 CC virus. IL-20 can be administered alone or in conjunction with radiation
 CC or chemotherapeutic agents or surgical excision of the involved cells or
 CC lesions
 CC
 XX
 SQ Sequence 176 AA;
 Query Match 100.0%; Score 910; DB 6; Length 176;
 Best Local Similarity 100.0%; Pred. No. 5e-88;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKASSLAFSLISAFFYLMTPTGTLNMGSCVIATNLQEIIRNGFSDIRGSVOAKDGI 60
 DB 1 MKASSLAFSLISAFFYLMTPTGTLNMGSCVIATNLQEIIRNGFSDIRGSVOAKDGI 60
 QY 61 DIRILRRTESTLODTKPNRCCILRLRLYLDRVFKNVOTPPHYTLRKISLSANSFLTK 120
 DB 61 DIRILRRTESTLODTKPNRCCILRLRLYLDRVFKNVOTPPHYTLRKISLSANSFLTK 120
 QY 121 KDRLCHAHMTCHGSEAMKKYSQILSHFEKLEPQAAVVKAAGELDIILQMEETE 176
 DB 121 KDRLCHAHMTCHGSEAMKKYSQILSHFEKLEPQAAVVKAAGELDIILQMEETE 176
 RESULT 7
 ID ABR00889 standard; protein; 176 AA.
 XX
 AC ABR00889;
 XX
 XX 15-JAN-2004 (first entry)
 XX
 DE Human cytokine-like polypeptide-10 (Zcyto10) #1.
 XX
 XX Human; cytokine-like polypeptide-10; Zcyto10; therapy; thrombocytopenia;
 KW autoimmune disease; insulin-dependent diabetes mellitus; immune response;
 KW rheumatoid arthritis; multiple sclerosis; infection; radiation therapy;
 KW asthma; bronchitis; wound healing; periodontal disease; antiinflammatory;
 KW psoriasis; eczema; dry skin; oral cavity; muscle atrophy; haemostatic;
 KW cancer; vulnerability.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..24
 FT Peptide /label= Signal_peptide

FT Protein 25. 176
 FT Disulfide-bond /note="Mature human Zcyto10"
 FT Disulfide-bond 33. 126
 FT Disulfide-bond 80. 132
 FT Disulfide-bond 81. 134
 XX US6576743-B1.
 PN 10-JUN-2003.
 PD
 XX
 PF 17-MAY-1999; 99US-00313458.
 XX
 XX 26-NOV-1997; 97US-0066597P.
 PR 25-NOV-1998; 98US-00199586.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Conklin DC, Haldeman BA;
 XX
 DR WPI; 2003-799828/75.
 XX N-PSDB; AAD61821.
 XX
 PT Novel human cytokine-like polypeptide-10, Zcyto10, useful for treating
 PT insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple
 PT sclerosis, asthma, psoriasis and inhibiting cancer cell growth.
 XX
 PS Claim 1; Col 31-32; Opp; English.

XX The invention relates to an isolated human cytokine-like polypeptide-10
 CC (Zcyto10) polypeptide. Zcyto10 is useful for prevention or treatment of
 CC conditions characterised by improper cell proliferation, cell
 CC differentiation or cytokine production. Zcyto10 is useful for treating
 CC autoimmune diseases such as insulin-dependent diabetes mellitus,
 CC rheumatoid arthritis, multiple sclerosis, etc., by inhibiting cellular
 CC immune response. The invention is useful for inhibiting cancer cell
 CC growth or proliferation, for stimulating immune system to combat
 CC microbial or viral infections, for increasing platelet production, and
 CC thus useful in cancer patients who experience thrombocytopenia due to
 CC cancer therapy or radiation therapy. Zcyto10 is useful in trachea-
 CC specific or tracheobronchial-specific applications, such as in the
 CC maintenance or would repair of the tracheobronchial epithelium or cells
 CC underlying the same, in regulating mucous production or mucociliary
 CC clearance of debris or in treatment of asthma, bronchitis or other
 CC diseases of the tracheobronchial tract. Zcyto10 may also enhance wound
 CC healing and promote regeneration of affected tissues which may be
 CC especially useful in the treatment of periodontal disease. Zcyto10 can be
 CC used to treat skin conditions such as psoriasis, eczema and dry skin in
 CC general. Zcyto10 is useful for regenerating gastrointestinal tract or
 CC oral cavity and for modulating muscle tone in the tracheobronchial tract,
 CC and for treating muscle atrophy in the elderly, sick or bed-ridden.
 CC Zcyto10 is also useful for promoting wound healing. The present sequence
 CC is human Zcyto10 protein
 XX

XX Sequence 176 AA;

Query Match 100.0%; Score 910; DB 7; Length 176;
 Best Local Similarity 100.0%; Pred. No. 56-86; Indels 0; Gaps 0;
 Matches 176; Conservative 0; Mismatches 0;

QY 1 MKASSLSAFLSLSAAFYLLMTPTSTGLKTLNLGSCVATNLQETIRNGFSIDIRGVSQAKDQNI 60
 DB 1 MKASSLSAFLSLSAAFYLLMTPTSTGLKTLNLGSCVATNLQETIRNGFSIDIRGVSQAKDQNI 60
 QY 61 DIRILARTESLQDTKPAANCCLRLRLRLYLDRVFNKYQTPDHYTLRKISLSLANSFLTIK 120
 DB 61 DIRILARTESLQDTKPAANCCLRLRLRLYLDRVFNKYQTPDHYTLRKISLSLANSFLTIK 120
 QY 121 KDLRLCHAHWTGCGEAMKKYSQILSHPEKLEPQAAVKAAGELDIILQMMEEET 176
 DB 121 KDLRLCHAHWTGCGEAMKKYSQILSHPEKLEPQAAVKAAGELDIILQMMEEET 176

RESULT 8

ADG46669
 ID ADG46669 standard; protein; 176 AA.
 XX
 AC ADG46669;
 XX
 XX 11-MAR-2004 (first entry)
 DT Human Zcyto10 protein #1.
 DE
 XX
 XX cytokine-like polypeptide-10; Zcyto10, wound healing;
 KW platelet proliferation; wound repair; mucous production; asthma;
 KW bronchitis; tracheobronchial tract disease; periodontal disease;
 KW skin condition; psoriasis; eczema; dry skin; protein therapy; human;
 KW vulnery; respiratory; antibronchitic; dental; dermatological.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Signal-peptide
 FT Protein 25..176
 PT /note="Human mature Zcyto10 protein"
 XX
 PN US2003176657-A1.
 XX
 PD 18-SEP-2003.
 XX
 PF 15-APR-2003; 2003US-00413661.
 XX
 PR 26-NOV-1997; 97US-0066597P.
 PR 25-NOV-1998; 98US-00199586.
 PR 17-MAY-1999; 99US-00313458.
 XX

XX (CONK/) CONKLIN D C.
 PA (HALD/) HALDEMAN B A.
 XX
 PI Conklin DC, Haldeman BA;
 XX
 DR WPI; 2003-863865/80.
 XX N-PSDB; ADG46668.
 XX

PT Novel isolated mammalian cytokine-like polypeptide-10 (Zcyto10), useful
 PT for treating asthma, bronchitis and other tracheobronchial damage.
 XX
 PS Claim 1, SEQ ID NO 2; 31pp; English.

XX The present invention relates to novel mammalian cytokine-like
 CC polypeptide-10 (Zcyto10) proteins and polynucleotides encoding such
 CC proteins. Sequences of the invention are useful for promoting the healing
 CC of wounds and for stimulating the proliferation of platelets in
 CC particular Zcyto10 polypeptides may be used in trachea-specific or
 CC tracheobronchial-specific applications such as maintenance or wound
 CC repair of the tracheobronchial epithelium or cells underlying it; in
 CC regulating mucous production; mucociliary clearance of debris; in
 CC treatment of asthma, bronchitis and other diseases of the
 CC tracheobronchial tract. They are also used to promote regeneration of
 CC affected tissues which may be especially useful in the treatment of
 CC periodontal disease. Zcyto10 polypeptides can be used to treat skin
 CC conditions such as psoriasis, eczema and dry skin in general. They are
 CC also used in protein therapy. The present sequence is human Zcyto10
 CC protein.
 CC
 XX

XX Sequence 176 AA;

Query Match 100.0%; Score 910; DB 7; Length 176;
 Best Local Similarity 100.0%; Pred. No. 56-88; Indels 0; Gaps 0;
 Matches 176; Conservative 0; Mismatches 0;

QY 1 MKASSLSAFLSLSAAFYLLMTPTSTGLKTLNLGSCVATNLQETIRNGFSIDIRGVSQAKDQNI 60
 DB 1 MKASSLSAFLSLSAAFYLLMTPTSTGLKTLNLGSCVATNLQETIRNGFSIDIRGVSQAKDQNI 60
 QY 61 DIRILARTESLQDTKPAANCCLRLRLRLYLDRVFNKYQTPDHYTLRKISLSLANSFLTIK 120
 DB 61 DIRILARTESLQDTKPAANCCLRLRLRLYLDRVFNKYQTPDHYTLRKISLSLANSFLTIK 120

Db 61 DIRILRTESLDTPKPNRCCLRHILRLYLDRVFKNYQTPDHYTLRKISSIANSPLTIK 120
 QY 121 KDRLCHAMTCHCGSEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
 Db 121 KDRLCHAMTCHCGSEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 9
 ADJ83281 standard; protein; 176 AA.
 ID ADJ83281;
 XX ADJ83281;
 AC ADJ83281;
 XX ADJ83281;
 DT 06-MAY-2004 (first entry)
 XX 06-MAY-2004 (first entry)
 DE Human interleukin IL-20 protein - SEQ ID 1.
 XX Human interleukin IL-20 protein - SEQ ID 1.
 KW inflammation; single chain antibody; interleukin; IL-20; IL-20RA subunit;
 KM IL-20RB subunit; antiinflammatory; dermatological; antipsoriatic;
 KM antiarthritic; respiratory; antiasthmatic; antilucer; antibacterial;
 KM immunosuppressive; gastrointestinal; skin; psoriasis; eczema;
 KM atopic dermatitis; contact dermatitis; lung;
 KM adult respiratory distress syndrome; asthma; bronchitis; pneumonia;
 KM arthritis; septic shock; multiple organ failure; bowel;
 KM ulcerative colitis; Crohn's disease; human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX US2004005320-A1.
 PN US2004005320-A1.
 XX 08-JAN-2004.
 PD 08-JAN-2004.
 XX 28-APR-2003; 2003US-00424658.
 PF 28-APR-2003; 2003US-00424658.
 XX 23-DEC-1999; 99US-0171969P.
 PR 22-JUN-2000; 2000US-0213341P.
 PR 22-DEC-2000; 2000US-00746359.
 XX 23-DEC-1999; 99US-0171969P.
 PR 22-JUN-2000; 2000US-0213341P.
 PR 22-DEC-2000; 2000US-00746359.
 XX (THOM/) THOMPSON P.
 PA (FOST/) FOSTER D C.
 PA (XUMW/) XU W.
 PA (MADD/) MADDEN K L.
 PA (KEL/) KELLY J D.
 PA (SPRE/) SPRECHER C A.
 PA (BLUM/) BLUMBERG H.
 PA (EAGAN/) EAGAN M A.
 PA (JASP/) JASPERS S R.
 PA (CHAN/) CHANDRASEKHAR Y A.
 PA (NOVA/) NOVAK J E.
 XX Thompson P, Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA;
 PI Blumberg H, Eagan MA, Jaspers SR, Chandrasekhar YA, Novak JE;
 XX WPI; 2004-081696/08.
 DR WPI; 2004-081696/08.
 XX Reducing or treating inflammation, e.g. inflammatory lung disease,
 PT comprises administering an antibody, antibody fragment or single chain
 PT antibody that specifically binds to an interleukin (IL)-20RA subunit of
 PT an IL-20 receptor.
 XX Disclosure; SEQ ID NO 1; 69pp; English.
 XX The invention relates to a novel method of reducing or treating
 CC inflammation in a mammal which comprises administering an antibody,
 CC antibody fragment or single chain antibody specifically binds to a
 CC receptor of interleukin (IL)-20 comprising an IL-20RA subunit and an IL-
 CC 20RB subunit. The method of the invention has antiinflammatory,
 CC dermatological, antipsoriatic, antiarthritic, respiratory, antiasthmatic,
 CC antilucer, antibacterial, immunosuppressive and gastrointestinal
 CC applications and may be useful for reducing or treating inflammation,
 CC including an inflammatory skin disease such as psoriasis, eczema, atopic
 CC dermatitis and contact dermatitis or an inflammatory lung disease such as

CC adult respiratory distress syndrome, asthma, bronchitis and pneumonia, as
 CC well as arthritis, septic shock, multiple organ failure, inflammatory
 CC bowel disease, ulcerative colitis or Crohn's disease. The current
 CC sequence is that of the human IL-20 protein of the invention.
 XX Sequence 176 AA;
 SQ Sequence 176 AA;
 Query Match 100.0%; Score 910; DB 8; Length 176;
 Best Local Similarity 100.0%; Pred. No. 5e-88;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKASSLAFSLLSAFAFLMTPTSGLKTINLGSQVIAITNLOEIRNGFSIDIRGSVQADGNI 60
 Db 1 MKASSLAFSLLSAFAFLMTPTSGLKTINLGSQVIAITNLOEIRNGFSIDIRGSVQADGNI 60
 QY 61 DIRILRTESLDTPKPNRCCLRHILRLYLDRVFKNYQTPDHYTLRKISSIANSPLTIK 120
 Db 61 DIRILRTESLDTPKPNRCCLRHILRLYLDRVFKNYQTPDHYTLRKISSIANSPLTIK 120
 QY 121 KDRLCHAMTCHCGSEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176
 Db 121 KDRLCHAMTCHCGSEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 10
 ADM95041 standard; protein; 176 AA.
 ID ADM95041;
 XX ADM95041;
 AC ADM95041;
 XX ADM95041;
 DT 17-JUN-2004 (first entry)
 XX 17-JUN-2004 (first entry)
 DE Human Interleukin-20 (IL-20) protein SeqID3.
 XX Human Interleukin-20 (IL-20) protein SeqID3.
 KM colon cancer; interleukin 20 receptor alpha chain;
 KM IL-20 receptor alpha chain; cycostatic; human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX JP2004075569-A.
 PN JP2004075569-A.
 XX 11-MAR-2004.
 PD 11-MAR-2004.
 XX 12-AUG-2002; 2002JP-00234880.
 PF 12-AUG-2002; 2002JP-00234880.
 XX 12-AUG-2002; 2002JP-00234880.
 PR 12-AUG-2002; 2002JP-00234880.
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX WPI; 2004-320878/30.
 DR WPI; 2004-320878/30.
 DR N-PSDB; ADM95042.
 XX Agent useful for prevention and/or treatment of colon cancer, comprises
 PT Interleukin 20 (IL-20), IL-20 receptor alpha chain, IL-20 receptor beta
 PT chain.
 XX Disclosure; SEQ ID NO 9; 50pp; Japanese.
 XX This invention relates to a novel agent for prevention and/or treatment
 CC of colon cancer, comprising of the interleukin 20 (IL-20) receptor alpha
 CC chain, its partial peptide or salt. The invention may be useful for the
 CC development of compounds with a cyrostatic activity. The invention is
 CC useful for preventing and/or treating colon cancer. A diagnostic agent is
 CC useful for diagnosis of colon cancer. By using IL-20, IL-20 receptor, its
 CC salt or its peptide, compounds that have altered binding property towards
 CC them can be efficiently screened. The present sequence is that of the
 CC human Interleukin-20 protein which is related to the invention.
 XX Sequence 176 AA;
 SQ Sequence 176 AA;
 Query Match 100.0%; Score 910; DB 8; Length 176;
 Best Local Similarity 100.0%; Pred. No. 5e-88;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLAFSLSAFYLLMTPSTGLKTNLNGSCVATNLOEIRNGFSDIRGSVOAKDGN 60
 DB 1 MKASSLAFSLSAFYLLMTPSTGLKTNLNGSCVATNLOEIRNGFSDIRGSVOAKDGN 60
 QY 61 DIRILRRTESLQDTKPNARCCLRLRLRLYLDRVFNKYQTPDHYTLRKISSLSANSPFLTK 120
 DB 61 DIRILRRTESLQDTKPNARCCLRLRLRLYLDRVFNKYQTPDHYTLRKISSLSANSPFLTK 120
 QY 121 KDLRLCHAMHTCHGCEBAMKKYSQILSHPEKLEPQAAVVKALGELDILLQWMEETE 176
 DB 121 KDLRLCHAMHTCHGCEBAMKKYSQILSHPEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 11
 ADQ88067
 ID ADQ88067 standard; protein; 176 AA.
 AC ADQ88067;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human Zcyto10 longer form protein.
 XX
 KW Mammalian cytokine-like polypeptide-10; Zcyto10; cell proliferation;
 KW cell differentiation; cytokine production; autoimmune disease;
 KW insulin dependent diabetes mellitus; multiple sclerosis;
 KW rheumatoid arthritis; cancer; wound healing; tissue regeneration;
 KW platelet count; asthma; skin disease; psoriasis; eczema; dry skin;
 KW antidiabetic; neuroprotective; antirheumatic; antiarthritic; cytostatic;
 KW immunostimulant; vulnary; antiaesthetic; antiporiatic; dermatological;
 KW gene therapy; human.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Signal_peptide 25..176
 FT Disulfide-bond /note="Human mature Zcyto10 protein" 33..126
 FT Disulfide-bond /note = Intramolecular disulfide bond 80..132
 FT Disulfide-bond /note = Intramolecular disulfide bond 81..134
 FT Disulfide-bond /note = Intramolecular disulfide bond
 XX
 PN US2004142428-A1.
 XX
 PD 22-JUL-2004.
 XX
 PF 27-FEB-2004; 2004US-00789129.
 XX
 PR 26-NOV-1997; 97US-0066597P.
 PR 25-NOV-1998; 98US-00199586.
 PR 15-APR-2003; 2003US-00413661.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Conklin DC, Haldeman BA;
 XX
 DR WPI; 2004-552564/53.
 DR N-PsDB; ADQ88066.
 XX
 XX New Zcyto10 polypeptides and polynucleotides, useful for treating
 PT autoimmune diseases (e.g. insulin dependent diabetes mellitus, multiple
 PT sclerosis or rheumatoid arthritis), or skin conditions (e.g. psoriasis or
 PT eczema).
 XX
 PS Claim 1; SEQ ID NO 2; 31pp; English.
 XX
 CC The present invention provides mammalian cytokine-like polypeptide-10
 CC (Zcyto10) proteins and their encoding polynucleotides. The invention is

CC useful for treating conditions characterized by improper cell
 CC proliferation, cell differentiation or cytokine production, specifically
 CC for treating autoimmune diseases such as insulin dependent diabetes
 CC mellitus, multiple sclerosis and rheumatoid arthritis and for inhibiting
 CC cancer cell growth. The invention is also used to stimulate the immune
 CC system, to enhance wound healing and promote regeneration of affected
 CC tissues, to increase platelet count and to treat asthma and skin
 CC conditions such as psoriasis, eczema and dry skin. The invention acts as
 CC an antidiabetic, neuroprotective, antirheumatic, antiarthritic,
 CC cytostatic, immunostimulant, vulnary, antiaesthetic, antiporiatic and
 CC dermatological agent. The invention is also used in gene therapy. The
 CC present sequence is human Zcyto10 longer form protein.
 XX
 SO Sequence 176 AA;
 QY Query Match 100.0%; Score 910; DB 8; Length 176;
 DB Best Local Similarity 100.0%; Pred. No. 5e-88;
 DB Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKASSLAFSLSAFYLLMTPSTGLKTNLNGSCVATNLOEIRNGFSDIRGSVOAKDGN 60
 DB 1 MKASSLAFSLSAFYLLMTPSTGLKTNLNGSCVATNLOEIRNGFSDIRGSVOAKDGN 60
 QY 61 DIRILRRTESLQDTKPNARCCLRLRLRLYLDRVFNKYQTPDHYTLRKISSLSANSPFLTK 120
 DB 61 DIRILRRTESLQDTKPNARCCLRLRLRLYLDRVFNKYQTPDHYTLRKISSLSANSPFLTK 120
 QY 121 KDLRLCHAMHTCHGCEBAMKKYSQILSHPEKLEPQAAVVKALGELDILLQWMEETE 176
 DB 121 KDLRLCHAMHTCHGCEBAMKKYSQILSHPEKLEPQAAVVKALGELDILLQWMEETE 176

RESULT 12
 ADR16328
 ID ADR16328 standard; protein; 176 AA.
 AC ADR16328;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human cytokine-like polypeptide-10 (Zcyto10) long form protein.
 XX
 KW Cytokine-like polypeptide-10; Zcyto10; therapy; asthma; infection;
 KW psoriasis; eczema; dry skin; wound healing; platelet proliferation;
 KW human.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Signal_peptide 25..176
 FT Disulfide-bond /note="Mature Zcyto10 long form protein" 33..126
 FT Disulfide-bond 80..132
 FT Disulfide-bond 81..134
 XX
 PN US2004152878-A1.
 XX
 PD 05-AUG-2004.
 XX
 PF 27-FEB-2004; 2004US-00789968.
 XX
 PR 26-NOV-1997; 97US-0066597P.
 PR 25-NOV-1998; 98US-00199586.
 PR 15-APR-2003; 2003US-00413661.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Conklin DC, Haldeman BA;
 XX
 DR WPI; 2004-580197/56.
 DR N-PsDB; ADR16327.
 XX

```
XX New isolated antibody that binds to a Zcyto10 polypeptide, useful for
PT treating asthma, microbial or viral infections, and for promoting the
PT healing of wounds, psoriasis, eczema or dry skin.
XX
PS Claim 1; SEQ ID NO 2; 32pp; English.
XX
CC The invention relates to novel cytokine-like polypeptide-10 (Zcyto10)
CC polypeptides and polynucleotides. Zcyto10 sequences are useful for
CC treating asthma, microbial or viral infections, psoriasis, eczema or dry
CC skin, for promoting the healing of wounds and for stimulating the
CC proliferation of platelets. The present sequence is human Zcyto10
CC protein.
XX
SQ Sequence 176 AA;

Query Match          100.0%; Score 910; DB 8; Length 176;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLAFSLLSAFAFYLLMTPTSTGLKTLNLSGVATNLOEIRNGSPDIRGSVOAKDGN 60
    |||||
DB 1 MKASSLAFSLLSAFAFYLLMTPTSTGLKTLNLSGVATNLOEIRNGSPDIRGSVOAKDGN 60
    |||||

QY 61 DIRILRTESLQDTKPNRCCILRHLLRLYLDRVFKNYQTPDHYTLRKISSLSNSFLTIR 120
    |||||
DB 61 DIRILRTESLQDTKPNRCCILRHLLRLYLDRVFKNYQTPDHYTLRKISSLSNSFLTIR 120
    |||||

QY 121 KDIRLCHAHMTCHGGEAMKKYSQILSHFEKLEPQAAVKALGELDLILQMMEETE 176
    |||||
DB 121 KDIRLCHAHMTCHGGEAMKKYSQILSHFEKLEPQAAVKALGELDLILQMMEETE 176
    |||||

RESULT 13
ADSI8363
ID ADSI8363 standard; protein; 176 AA.
XX
AC ADSI8363;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human Zcyto10 protein #1.
XX
KW Zcyto10; cytokine-like polypeptide; cell proliferation;
KW cell differentiation; autoimmune disease; diabetes; multiple sclerosis;
KW rheumatoid arthritis; asthma; psoriasis; cancer; wound; gene therapy;
KW immunosuppressive; antidiabetic; neuroprotective; antineumatic;
KW antiarthritic; antiasthmatic; antiportalatic; cyostatic; vulnery;
KW human.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FH 1..24
XX PT Peptide /label= Signal_peptide
XX PT 25..176
XX PT Protein /note= "Mature Zcyto10 protein"
XX FT Disulfide-bond 33..126
XX FT Region 35
XX FT /note= "Helix A"
XX FT Region 49
XX FT /note= "Helix A"
XX FT Region 91
XX FT /note= "Helix B"
XX FT Region 105
XX FT /note= "Helix B"
XX FT Region 112
XX FT /note= "Helix C"
XX FT Region 126
XX FT /note= "Helix C"
XX FT Region 158
XX FT /note= "Helix C"
XX FT Region 172
XX FT /note= "Helix D"
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```
FT /note= "Helix D"
XX
XX US2004181040-A1.
XX
XX 16-SEP-2004.
XX
XX 29-DEC-2003; 2003US-00748484.
XX
XX 26-NOV-1997; 97US-0066597P.
XX 25-NOV-1998; 98US-00199586.
XX 15-APR-2003; 2003US-00413661.
XX
XX (CONK/) CONKLIN D C.
XX (HALD/) HALDEMAN B A.
XX (GROS/) GROSSMANN A.
XX
XX Conklin DC, Haldeman BA, Grossmann A;
XX
XX WPI; 2004-667683/65.
XX N-PSDB; ADSI8362.
XX
XX New antibody that selectively binds to a Zcyto10 polypeptide useful for
PT modulating cell proliferation, cell differentiation or cytokine
PT production in the prevention or treatment of e.g. autoimmune diseases,
PT cancer or wounds.
XX
XX Claim 1; SEQ ID NO 2; 31pp; English.
XX
XX The present invention relates to a mammalian cytokine-like polypeptide,
CC Zcyto10 and its encoding polynucleotide. The invention is useful for
CC modulating cell proliferation, cell differentiation or cytokine
CC production in the prevention or treatment of conditions such as
CC autoimmune diseases (e.g. diabetes, multiple sclerosis, rheumatoid
CC arthritis, asthma or psoriasis) and cancer or wounds. The invention is
CC also useful in gene therapy. The present sequence is the human Zcyto10
CC protein.
XX
SQ Sequence 176 AA;

Query Match          100.0%; Score 910; DB 8; Length 176;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLAFSLLSAFAFYLLMTPTSTGLKTLNLSGVATNLOEIRNGSPDIRGSVOAKDGN 60
    |||||
DB 1 MKASSLAFSLLSAFAFYLLMTPTSTGLKTLNLSGVATNLOEIRNGSPDIRGSVOAKDGN 60
    |||||

QY 61 DIRILRTESLQDTKPNRCCILRHLLRLYLDRVFKNYQTPDHYTLRKISSLSNSFLTIR 120
    |||||
DB 61 DIRILRTESLQDTKPNRCCILRHLLRLYLDRVFKNYQTPDHYTLRKISSLSNSFLTIR 120
    |||||

QY 121 KDIRLCHAHMTCHGGEAMKKYSQILSHFEKLEPQAAVKALGELDLILQMMEETE 176
    |||||
DB 121 KDIRLCHAHMTCHGGEAMKKYSQILSHFEKLEPQAAVKALGELDLILQMMEETE 176
    |||||

RESULT 14
ADV66904
ID ADV66904 standard; protein; 176 AA.
XX
AC ADV66904;
XX
DT 24-FEB-2005 (first entry)
XX
DE Human IL-20 wild-type, SEQ ID 20.
XX
XX Dermatological; Antiinflammatory; Interleukin-20 antagonist;
KW Interleukin-20; IL-20; cytokine; dermatological disease; inflammation.
XX
XX Homo sapiens.
XX
XX OS
XX PN US2004248097-A1.
XX
```

PD 09-DEC-2004.
 XX 23-MAY-2003; 2003US-00444765.
 PF 23-MAY-2003; 2003US-00444765.
 XX
 XX 23-MAY-2003; 2003US-00444765.
 PA (CHAN/) CHANG M.
 PI Chang M.
 XX
 XX WPI, 2005-072805/08.
 DR
 XX New interleukin-20 alternatively spliced polypeptides, useful for
 PT increasing the level of interleukin-6, tumor necrosis factor-alpha,
 PT keratinocyte growth factor-1 or reactive oxygen species in a cell.
 XX
 PS Disclosure; SEQ ID NO 20; 27pp; English.
 XX
 XX The present invention relates to alternatively spliced interleukin (IL)-
 CC 20 variants (I; ADV66885 and ADV66902) and promoter sequences (II;
 CC ADV66887-ADV66901). IL-20 is a member of the IL-10 family of cytokines.
 CC Members in this family are important in controlling inflammation
 CC responses. (I) is useful for increasing the level of IL-6, Tumor Necrosis
 CC Factor (TNF)-alpha, Keratinocyte Growth Factor-1 (KGF-1) or reactive
 CC oxygen species in a cell, which involves contacting (I) with a cell. (II)
 CC is useful for identifying a compound for treating an IL-20-induced
 CC disease, which involves contacting a compound with a cell containing a
 CC nucleic acid comprising IL-20 promoter operably linked to a reporter
 CC gene, and determining the expression level of the reporter gene in the
 CC cell, where the expression level of the reporter gene in the presence of
 CC the compound, if lower than that in the absence of the compound,
 CC indicates that the compound is a candidate for treating IL-20 induced
 CC disease. The IL-20-induced disease is a skin disease or an inflammatory
 CC disease. The present sequence is the wild-type human IL-20 sequence,
 CC which was used in an alignment with the alternatively spliced human IL-20
 CC variant sequence.
 XX
 SQ Sequence 176 AA;

Query Match 100.0%; Score 910; DB 9; Length 176;
 Best Local Similarity 100.0%; Pred. No. 5e-88;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLAFSLSAAFYLLMTPTSTGLKTLNLSGVATNLQEIIRNGFSDIRGSVQAKDGI 60
 DB 1 MKASSLAFSLSAAFYLLMTPTSTGLKTLNLSGVATNLQEIIRNGFSDIRGSVQAKDGI 60
 QY 61 DIRIIRRTESLQDTKPARNCCLRLRLYLDRVFKNYQTPDHYTLRKISSLSANSLFLTK 120
 DB 61 DIRIIRRTESLQDTKPARNCCLRLRLYLDRVFKNYQTPDHYTLRKISSLSANSLFLTK 120
 QY 121 KDLRLCHAMTCHCGEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQNMEEETE 176
 DB 121 KDLRLCHAMTCHCGEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQNMEEETE 176

RESULT 15

ADM64518
 ID ADM64518 standard; protein; 176 AA.

XX ADM64518;

XX 24-MAR-2005 (first entry)

XX Human IL-20 protein, seqid:1.

XX Therapy; cns-gen.; respiratory-gen.; antiasthmatic; antipsoriatic;
 KW antiinflammatory; psoriasis; dermatological disease; immune disorder;
 KW pulmonary disease; asthma; inflammation; respiratory disease; bronchitis;
 KW antiinflammatory; inflammation; cystic fibrosis;
 KW gastrointestinal disease; chemotherapy; interleukin.
 XX
 OS Homo sapiens.

XX US2005003475-A1.
 PN
 XX 06-JAN-2005.
 PD
 XX 22-DEC-2000; 2000US-00745792.
 PF 23-DEC-1999; 99US-0171966P.
 XX 22-JUN-2000; 2000US-0213416P.
 PR
 XX (FOST/) FOSTER D C.
 PA (XUWV/) XU W.
 PA (MADD/) MADDEN K L.
 PA (KELL/) KELLY J D.
 PA (SPRE/) SPEICHER C A.
 PA (BRAN/) BRANDT C S.
 PA (RIXO/) RIXON M W.
 PA (PRES/) PRESNEL S R.
 PA (FOX B/) FOX B A.
 XX
 PI Foster DC, Xu W, Madden KL, Kelly JD, Sprecher CA, Brandt CS;
 PI Rixon MW, Presnell SR, Fox BA;
 XX
 XX WPI, 2005-065240/07.
 DR
 XX
 XX New isolated soluble receptor comprised of an interleukin 20 receptor
 PT alpha (IL-20RA) subunit and a IL-20RB subunit, useful for treating
 PT inflammatory diseases e.g., psoriasis and inflammatory lung diseases
 PT e.g., asthma.
 XX
 PS Disclosure; SEQ ID NO 1; 73pp; English.
 XX
 CC The present invention relates to an soluble receptor having an
 CC interleukin 20 receptor alpha (IL-20RA) subunit and an IL-20RB subunit.
 CC The invention is useful for treating inflammatory diseases such as
 CC psoriasis and inflammatory lung diseases such as asthma, bronchitis and
 CC cystic fibrosis. The present sequence is the human IL-20 protein.
 XX
 SQ Sequence 176 AA;

Query Match 100.0%; Score 910; DB 9; Length 176;
 Best Local Similarity 100.0%; Pred. No. 5e-88;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLAFSLSAAFYLLMTPTSTGLKTLNLSGVATNLQEIIRNGFSDIRGSVQAKDGI 60
 DB 1 MKASSLAFSLSAAFYLLMTPTSTGLKTLNLSGVATNLQEIIRNGFSDIRGSVQAKDGI 60
 QY 61 DIRIIRRTESLQDTKPARNCCLRLRLYLDRVFKNYQTPDHYTLRKISSLSANSLFLTK 120
 DB 61 DIRIIRRTESLQDTKPARNCCLRLRLYLDRVFKNYQTPDHYTLRKISSLSANSLFLTK 120
 QY 121 KDLRLCHAMTCHCGEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQNMEEETE 176
 DB 121 KDLRLCHAMTCHCGEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQNMEEETE 176

Search completed: December 24, 2005, 10:42:59
 Job time : 187 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 24, 2005, 10:39:36 ; Search time 38 seconds

(without alignments)
445.636 Million cell updates/sec

Title: US-10-789-129-2

Perfect score: 910

Sequence: 1 MKASSIAFSLSAFYLLWT.....AVVKALGELDLLQNMETE 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 156.5 | 17.2 | 178 | 2 A38580 | interleukin-10 pre |
| 2 | 155 | 17.0 | 170 | 1 Q0B52 | BCRF1 protein - hu |
| 3 | 155 | 17.0 | 175 | 2 I46591 | interleukin 10 - p |
| 4 | 147.5 | 16.2 | 179 | 2 A48558 | interleukin 10 hom |
| 5 | 144 | 15.8 | 178 | 2 A34853 | interleukin-10 pre |
| 6 | 136 | 14.9 | 178 | 2 JN0475 | interleukin-10 pre |
| 7 | 94.5 | 10.4 | 567 | 2 UCS538 | Rab geranylgeranyl |
| 8 | 94.5 | 10.4 | 567 | 2 A45977 | Rab geranylgeranyl |
| 9 | 93.5 | 10.3 | 809 | 2 S64594 | probable beta-adap |
| 10 | 85 | 9.3 | 140 | 2 F83128 | probable transcrip |
| 11 | 81.5 | 9.0 | 646 | 2 T33346 | hypothetical prote |
| 12 | 81 | 8.9 | 1062 | 2 S46367 | protein kinase CDC |
| 13 | 80 | 8.8 | 542 | 2 T19925 | hypothetical prote |
| 14 | 76.5 | 8.4 | 502 | 2 AD3160 | hypothetical prote |
| 15 | 76.5 | 8.4 | 553 | 2 B90153 | 2-isopropylmalate |
| 16 | 76 | 8.4 | 523 | 2 S64826 | probable membrane |
| 17 | 76 | 8.4 | 917 | 2 T21870 | hypothetical prote |
| 18 | 75 | 8.2 | 276 | 2 B71517 | probable synectoch |
| 19 | 75 | 8.2 | 726 | 2 T46023 | ATP-dependent RNA |
| 20 | 75 | 8.2 | 729 | 2 H84912 | probable pre-mRNA |
| 21 | 74.5 | 8.2 | 121 | 2 E83640 | hypothetical prote |
| 22 | 74.5 | 8.2 | 1047 | 2 D71302 | probable exonuclea |
| 23 | 74 | 8.1 | 682 | 1 H69879 | ATP-dependent DNA |
| 24 | 73.5 | 8.1 | 449 | 2 B71917 | udp-n-acetylmurama |
| 25 | 73.5 | 8.1 | 653 | 2 D87602 | sensory box histid |
| 26 | 73.5 | 8.1 | 729 | 2 F97321 | membrane export pr |
| 27 | 73.5 | 8.1 | 782 | 2 S33945 | late protein, 100K |
| 28 | 73.5 | 8.1 | 794 | 2 A98211 | hypothetical prote |
| 29 | 73.5 | 8.1 | 794 | 2 C86057 | hypothetical prote |

| | | | | | |
|----|------|-----|------|----------|---------------------|
| 30 | 73 | 8.0 | 471 | 2 B38637 | Ras inhibitor (c10 |
| 31 | 73 | 8.0 | 563 | 2 D90531 | exonuclease ABC s |
| 32 | 73 | 8.0 | 614 | 2 E83880 | hypothetical prote |
| 33 | 73 | 8.0 | 1008 | 2 D84434 | probable receptor- |
| 34 | 72.5 | 8.0 | 261 | 2 H98213 | transcription repr |
| 35 | 72.5 | 8.0 | 388 | 2 T00641 | hypothetical prote |
| 36 | 72.5 | 8.0 | 409 | 2 A54750 | TNF receptor assoc |
| 37 | 72.5 | 8.0 | 447 | 2 T20552 | hypothetical prote |
| 38 | 72.5 | 8.0 | 481 | 2 S39682 | lydb. protein - Bac |
| 39 | 72.5 | 8.0 | 1101 | 2 T33153 | hypothetical prote |
| 40 | 72.5 | 8.0 | 2182 | 2 T28634 | variant-specific s |
| 41 | 72.5 | 8.0 | 2581 | 2 AF2545 | hypothetical prote |
| 42 | 72 | 7.9 | 255 | 2 F81833 | conserved hypotet |
| 43 | 72 | 7.9 | 279 | 2 E81197 | hypothetical prote |
| 44 | 72 | 7.9 | 279 | 2 A70081 | conserved hypotet |
| 45 | 72 | 7.9 | 351 | 2 S74651 | hypothetical prote |

ALIGNMENTS

RESULT 1
A38580
interleukin-10 precursor - human
N:Alternate names: cytokine synthesis inhibitory factor (CSIF) ; IL-10
C:Species: Homo sapiens (man)
C>Date: 14-Feb-1992 #sequence revision 14-Feb-1992 #text_change 09-Jul-2004
C:Accession: A38580; GI1539; S49110; 137890
R:Vieira, P.; de Waal-Malefyt, R.; Dang, M.N.; Johnson, K.E.; Kastelein, R.; Fiorentin
Proc. Natl. Acad. Sci. U.S.A. 88, 1172-1176, 1991
A>Title: Isolation and expression of human cytokine synthesis inhibitory factor cDNA c
A:Reference number: A38580; MUID:91142134; PMID:1847510
A:Accession: A38580
A:Molecule type: mRNA
A:Residues: 1-178 <VIB>
A:Cross-references: UNIPROT:P22301; UNIPARC:UP10000034E50; GB:M57627; NID:g186270; PID
R:Kinsbor, W.T.; Syto, R.; Tsaropoulos, A.; Zhang, R.; Durkin, J.; Baldwin, S.; Paliw
Biochemistry 32, 8807-8815, 1993
A>Title: Disulfide bond assignments and secondary structure analysis of human and murin
A:Reference number: A48693; MUID:93372085; PMID:8364028
A:Contents: annotation; disulfide bonds in recombinant protein
R:Sanjanwala, B.
A:Reference number: EMBL Data Library, October 1994
A:Accession: G07695
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-178 <SAN>
A:Cross-references: UNIPARC:UP10000034E50; EMBL:U16720; NID:g1041812; PIDN:AA60104.1;
R:Kube, D.; Platzer, C.; von Knechten, A.; Straub, H.; Hafner, M.; Teich, H.
submitted to the EMBL Data Library, March 1994
A:Description: Isolation of the human interleukin-10-promoter. Characterization of the
A:Reference number: S49110
A:Accession: S49110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6, 'PVWMS', <XUB>
A:Cross-references: UNIPARC:UP10000178477; EMBL:X78437; NID:g1167482
R:Platzer, C.; Volk, H.D.; Platzer, M.
DNA Seq. 4, 399-401, 1994
A>Title: 5' noncoding sequence of human IL-10 gene obtained by oligo-cassette PCR walk
A:Reference number: I37890; MUID:95143580; PMID:7841462
A:Accession: I37890
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <PLA>
A:Cross-references: UNIPARC:UP1000011B9B9; EMBL:X73536; NID:g452395; PIDN:CAA51942.1; I
C:Genetics:
A:Gene: GDB: IL10; IL-10
A:Cross-references: GDB:128636; OMIM:124092
A:Map position: 1q31-q32
A:Introns: 55/3; 75/3; 126/3; 148/3
C:Superfamily: interleukin-10

C/Keywords: cytokine; glycoprotein; lymphokine; T-cell
F/1-18/Domain: signal sequence #status predicted <SIG-
P/19-178/Product: interleukin-10 #status predicted <MKT>
P/30-126,80-132/Dissulfide bonds: #status experimental
F/134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.2%; Score 156.5; DB 2; Length 178;
Best Local Similarity 27.4%; Pred. No. 8.1e-08;
Matches 43; Conservative 32; Mismatches 71; Indels 11; Gaps 5;
QY 22 STGLKTLNIGSCV-----IATNLQIRNGFSDIRGSVOAKGNDIRILRRTESLQDTKP 76
19 SPFGQGSSENSCHFPENLPMRLDRAFSRVKTFPQMD-QLD-NLLKESLDEPKG 76
DB 77 ANRCLLRHLRLYLDRVFKNYQTPDHYTLRKISLSANSPFLTKDRLCHAMTCHGE 136
77 YLCCQALSEMIQFYLEEVMPQAEQNDPDIKAHVNSLGENIKTLRLRLRCHRFPC---E 133
QY 137 EAMKYSQILSHPEKLEPOAAVVKALGELDILLQWME 173
DB 134 NKSRAVEQVKNAPNKLQ-EKGIYKAMSEFDIFINYIE 169

RESULT 2

BCR1 protein - human herpesvirus 4 (strain B95-8)
C/Species: human herpesvirus 4, Epstein-Barr virus
C/Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C/Accession: A03741; S32974
R/Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A/Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A/Reference number: A93065; MUID:85035713; PMID:6092825
A/Accession: A03741
A/Molecule type: DNA
A/Residues: 1-170 <BAN>
A/Cross-references: UNIPROT:P03180; UNIPARC:UPI000000CDBE; EMBL:V01555; NID:959074; PIDN
R/Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A/Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A/Reference number: A03794; MUID:84270667; PMID:6087149
A/Contents: annotation; protein coding region
C/Superfamily: interleukin-10

Query Match 17.0%; Score 155; DB 1; Length 170;
Best Local Similarity 28.9%; Pred. No. 1.1e-07;
Matches 39; Conservative 29; Mismatches 61; Indels 6; Gaps 4;
QY 39 LQIRNGFSDIRGSVOAKGNDIRILRRTESLQDTKPANRCCLLRLHLRLYLDRVFKNY 98
DB 34 LRDRDAFSRVKTFPQMD-EVD-NLLKESLDEPKGYLGCQALSEMIQFYLEEVMPQ 91
QY 99 QTPDHYTLRKISLSANSPFLTKDRLCHAMTCHGEAMKYSQILSHPEKLEPOAAV 158
DB 92 ENQDPKADKVNLSIGELKTLRLRLRCHRFPC---ENKSKAVEQVKNAPNKLQ-EKGI 147
QY 159 VKALGELDILLQWME 173
DB 148 YKAMSEFDIFINYIE 162

RESULT 3

interleukin 10 - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: I46591
R/Biancho, G.; Gianello, P.; Germana, S.; Baetscher, M.; Sachs, D.H.; Leguern, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 2800-2804, 1995
A/Title: Molecular identification of porcine interleukin 10: regulation of expression in
A/Reference number: I46591; MUID:95224028; PMID:7708727
A/Accession: I46591
A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA
A/Residues: 1-175 <BLA>
A/Cross-references: UNIPROT:Q29055; UNIPARC:UPI000012D476; GB:I20001; NID:G309792; PIDN:
C/Genes:
A/Genes: 11-10
C/Superfamily: interleukin-10

Query Match 17.0%; Score 155; DB 2; Length 175;
Best Local Similarity 27.0%; Pred. No. 1.1e-07;
Matches 48; Conservative 34; Mismatches 78; Indels 18; Gaps 6;
QY 1 MKASSIAFSLSAAFYLLMTPETGKTLNIGSCV-----IATNLQIRNGFSDIRGSVOA 55
1 MESSALTYCLI-----FLAGVAASIKSEN--SCHFPPTSLPMMLRLRAAFPVVSPFT 53
DB 56 KQGNIDIRILRRTESLQDTKPANRCCLLRLHLRLYLDRVFKNYQTPDHYTLRKISLSAN 115
54 KQWQMD--LNLGSLLEDEPKGYLGCQALSEMIQFYLEDVMPRAESDGEDIKHVNLSGER 111
QY 116 FLTKDRLCHAMTCHGEAMKYSQILSHPEKLEPOAAVVKALGELDILLQWME 173
DB 112 LKTLRLRLRCHRFPC---ENKSKAVEQVKNAPNKLQ-ERGVYKAMSEFDIFINYIE 165

RESULT 4

A48558
interleukin 10 homolog - equine herpesvirus 2
N/Alternate names: hypothetical protein E7
C/Species: equine herpesvirus 2
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: A48558; S55664
R/Kode, H.J.; Janssen, W.; Rosen-Wolff, A.; Bugert, J.U.; Thein, P.; Becker, Y.; Darai,
Virus Genes 7, 111-116, 1993
A/Title: The genome of equine herpesvirus type 2 harbors an interleukin 10 (IL10)-like g
A/Reference number: A48558; MUID:93227565; PMID:8385838
A/Accession: A48558
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-179 <KOD>
A/Cross-references: UNIPROT:O89451; UNIPARC:UPI000012D058; GB:S59624; NID:G299468; PIDN
A/Note: sequence extracted from NCBI backbone (NCBIN:129334; NCBIPI:129335)
R/Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J Mol. Biol. 249, 520-528, 1995
A/Title: The DNA sequence of equine herpesvirus 2
A/Reference number: S55594; MUID:95302501; PMID:7783207
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-179 <TEL>
A/Cross-references: UNIPARC:UPI000012D058; GB:U20824; NID:G695172; PIDN:AAC13857.1; PID
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C/Superfamily: interleukin-10

Query Match 16.2%; Score 147.5; DB 2; Length 179;
Best Local Similarity 31.9%; Pred. No. 6.1e-07;
Matches 44; Conservative 24; Mismatches 59; Indels 11; Gaps 6;
QY 39 LQIRNGFSDIRGSVOAKGNDIRILRRTESLQDTKPANRCCLLRLHLRLYLDRVFKNY 98
DB 41 LHELRAAFSRVKTFFQMD-QLD-NMLDGSLLDEPKGYLGCQALSEMIQFYLEEVMP-- 96
QY 99 QTPDHYTLR---KISLSANSPFLTKDRLCHAMTCHGEAMKYSQILSHPEKLEPO 155
DB 97 QAEHSTDEKQKVNLSIGELKTLRLRLRCHRFPC---ENKSKAVEQVKNAPNKLQ-B 152
QY 156 AAVVKALGELDILLQWME 173
DB 153 KGVYKAMSEFDIFINYIE 170

RESULT 5

A34853
interleukin-10 precursor - mouse

N/Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10
 C/Species: Mus musculus (house mouse)
 C/Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
 C/Accession: A34853; 156136
 R/Moore, K.W.; Veleira, P.; Fiorentino, D.F.; Trounstein, M.L.; Khan, T.A.; Mosmann, T.R.
 Science 248, 1230-1234, 1990
 A/Title: Homology of cytokine synthesis inhibitory factor (IL-10) to the Epstein-Barr vi
 A/Reference number: A34853; PMID:90273182; PMID:2161559
 A/Accession: A34853
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-178 <MO>
 A/Cross-references: UNIPROT:P18893; UNIPARC:UP1000002149E; GB:M37897; NID:G198288; PIDN:
 R/Kim, J.M.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Khan, T.A.; Moore, K.W.
 J. Immunol. 148, 3638-3623, 1992
 A/Title: Structure of the mouse IL-10 gene and chromosomal localization of the mouse and
 A/Reference number: 156136; PMID:92268508; PMID:1350294
 A/Accession: 156136
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-178 <RES>
 A/Cross-references: UNIPARC:UP1000002149E; GB:M84340; NID:G198291; PIDN:AAA39275.1; PID:
 C/Genetics:
 A/Gene: IL10
 A/Introns: 55/3; 75/3; 126/3; 148/3
 C/Superfamily: interleukin-10
 C/Keywords: cytokine; lymphokine; T-cell

Query Match 15.8%; Score 144; DB 2; Length 178;
 Best Local Similarity 31.1%; Pred. No. 1.3e-06;
 Matches 42; Conservative 19; Mismatches 68; Indels 6; Gaps 4;

QY 39 LOEIRNGFSDIRGVAKGNDIRLRRTESLDTPKPNRCCLRLHRLVLDYRFRKXY 98
 Db 41 LLELRKRAFSQVKTFFQTKD-QLD-NILTDLSLMQDKYGCQALSEMIQFYLVEVWPA 98
 QY 99 QTPDHYTLRKISSIANSFLTIKKDLRLCHAHMTCHGCEBAMKXYSQLSHFEKLEPQAAY 158
 Db 99 EKKEPEIKKHINSLSGKMLTLRLRRLRCHRFPC---EKSKAVEQVKSDFNKLQDQ-GV 154
 QY 159 VVALGELDTLLQWME 173
 Db 155 YKAMNEFDIFINCIE 169

RESULT 6
 UN0475
 Interleukin-10 precursor - rat
 N/Alternate names: cytokine synthesis inhibitory factor
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: UN0475; JCI1357; S36021
 R/Feng, L.; Tang, W.W.; Chang, J.C.C.; Wilson, C.B.
 Biochem. Biophys. Res. Commun. 192, 452-458, 1992
 A/Title: Molecular cloning of rat cytokine synthesis inhibitory factor (IL-10) cDNA and
 A/Reference number: UN0475
 A/Accession: UN0475
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-178 <FEN>
 A/Cross-references: UNIPROT:P29456; UNIPARC:UP10000167959
 R/Goodman, R.E.; Oblak, J.; Bell, R.G.
 Biochem. Biophys. Res. Commun. 189, 1-7, 1992
 A/Title: Synthesis and characterization of rat interleukin-10 (IL-10) cDNA clones from c
 A/Reference number: JCI1357; PMID:93080542; PMID:1280414
 A/Accession: JCI1357
 A/Molecule type: mRNA
 A/Residues: 1, 'P', 3-64, 'L', 66-178 <GOO>
 A/Cross-references: UNIPARC:UP1000012D477; GB:L02926; NID:G204903; PIDN:AAA1425.1; PID:
 R/Feng, L.
 submitted to the EMBL Data Library, July 1991
 A/Reference number: S36021
 A/Accession: S36021

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-178 <FE2>
 A/Cross-references: UNIPARC:UP10000167959; EMBL:X60675; NID:G296620; PIDN:CAA43090.1;
 C/Superfamily: Interleukin-10
 C/Keywords: cytokine; glycoprotein; lymphokine; T-cell
 F/18/Domain: signal sequence #status predicted <Sig>
 F/19-178/Product: interleukin-10 #status predicted <MAT>
 F/29,134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 136; DB 2; Length 178;
 Best Local Similarity 28.5%; Pred. No. 8e-06;
 Matches 53; Conservative 26; Mismatches 77; Indels 30; Gaps 8;

QY 1 MKASSLAFSLSAAPFLMTPTSTGKTLNLSGVATN-----LQEIRNGFSD 48
 Db 1 MGSALCCLLLA-----GVKT-SKGSIRGDNCTHPVPSQTHMLRLRAFSQ 50
 QY 49 INGSVQAKGNDIRLRRTES-LDTPKPNRCCLRLHRLVLDYRFRKXY 107
 Db 51 VTFPQKXD-QLDNIVL--TDSLQDFKQYLCQALSEMIKRYLVEVWPAENHGEIKE 107
 QY 108 KISSIANSFLTIKKDLRLCHAHMTCHGCEBAMKXYSQLSHFEKLEPQAAYKALGELDI 167
 Db 108 HINSLSGKMLTLMIQLRCHRFPC---ENKSKAVEQVKNDFNKLQDK-GYKAMNEFDI 163
 QY 168 LQWME 173
 Db 164 FNCIE 169

RESULT 7
 JCS538
 Rab geranyl transferase (EC 2.5.1.-) alpha chain - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
 C/Accession: JCS538
 R/Song, H.J.; Rossi, A.; Cecil, R.; Kim, I.G.; Arzano, M.A.; Jang, S.I.; De Laurenzi, V
 Biochem. Biophys. Res. Commun. 235, 10-14, 1997
 A/Title: The genes encoding geranyl transferase alpha-subunit and transglutamin.
 A/Reference number: JCS538; PMID:9739427; PMID:9196026
 A/Accession: JCS538
 A/Molecule type: DNA
 A/Residues: 1-567 <SON>
 A/Cross-references: UNIPROT:Q92696; UNIPARC:UP1000013188E
 C/Comment: This protein is involved in cutaneous disease. The gene of this enzyme is p
 A/Gene: Rabg9ta
 A/Introns: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 41
 C/Keywords: transferase

Query Match 10.4%; Score 94.5; DB 2; Length 567;
 Best Local Similarity 25.8%; Pred. No. 0.35;
 Matches 49; Conservative 26; Mismatches 82; Indels 33; Gaps 9;

QY 1 MKASSLAFSLSAAPFLMTPTSTGKTLNLSGVATNLOE--INSGFSD--INSGVQA 55
 Db 304 LPAASLNDQLPQHTFRVWMTAGDVOK---ECVLLKRGQSGWCDSTTDEQLFRCELSV 358
 QY 56 KQGNIDIRLRRTESLDTPKPNRCCLRLHRLVLDYRFRKXYOT-----PDH 103
 Db 359 EKSTYLGSELBSCKEQLQLEPENKCKLTLILRAALDPLYEKTKLQYQTLKAVDPRK 418
 QY 104 YT---LRKISSIANSFLTIK---KDLRLCHAHMTCHGCEBAMKXYSQL-SH--FEKL 152
 Db 419 ATYLDLRSKFLSNSVLMKEVAEVRVLAHKDLTVLCHLEQLLTVTHLDSHRLRTL 478
 QY 153 EPQAAYVAL 162
 Db 479 PPALAAKRL 488

RESULT 8

A45977

Rab geranylgeranyl transferase component B alpha subunit - rat

C:/Species: Rattus norvegicus (Norway rat)

C:/Date: 15-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:/Accession: A45977

R./Armerstrong, S.A.; Seabra, M.C.; Sudhof, T.C.; Goldstein, J.L.; Brown, M.S.

J. Biol. Chem. 268, 12221-12229, 1993

A:/Title: CDNA cloning and expression of the alpha and beta subunits of rat Rab geranylge

A:/Reference number: A45977; MUID:93280201; PMID:8505342

A:/Accession: A45977

A:/Status: Preliminary

A:/Molecule type: mRNA; protein

A:/Residues: 1-567 <ARM>

A:/Cross-references: UNIPROT:Q08602; UNIPARC:UPI0000013188F; GB:S62096; NID:G385474; PIDN:

A:/Experimental source: brain

A:/Note: sequence extracted from NCBI backbone (NCBIN:133369, NCBI:P.133370)

Query Match 10.4%; Score 94.5; DB 2; Length 567;

Best Local Similarity 24.2%; Pred. No. 0.35; Indels 33; Gaps 8;

Matches 46; Conservative 31; Mismatches 80; Indels 33; Gaps 8;

QY 1 MKASIAFSLLSAFAFYLLWTPSTGLKTLNLSGCVIATNIOE--IRNGFSD--IRGSVQA 55

Db 304 LPASLINDQLPQHTFRVITWGSQK-----ECVILKDRPCWCRCOSATDEQLFRGELSV 358

QY 56 KQGNIDIRILRRTESLDDTPANRCCILRHLLRL-YIDRVFKNYQTPDHYT----- 105

Db 359 EKSTVLOSELESCKEIOLEPEKMKCLITITILRLALDPLLYKETLQVYSTKKAVDPMR 418

QY 106 -----LRKISLANSFLTIK---KDLRLCHAMTCHGCEAMKKYSOI-LSH--FEKL 152

Db 419 AAVLUDLRSKFLLENSVLKMEYADVRLHLAKDILTVLCHLEQLLVTHLDLSHNRLLAL 478

QY 153 EPQAAVVKAL 162

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

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QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 479 PPALALRCL 488

Db 479 PPALALRCL 488

QY 62 IRI-----LRRTESLDDTPANRCCILRHLLRL-YIDRVFKNYQTPDHYTIRKISLANSFL 117

Db 79 VOLLYADVVKNITTTDTR-----VKRLIHLYLRFAPEN---DNLTLTSLNSLOKSIS 128

QY 118 TIKDRLCHAMTCHGCEAMKKYSQILSHPEK---LEPOA-----AVVK--ALGE 164

Db 129 DSNSELR-CFA--LSALSMKSSIAPIILHTVVKLVDPDSAMVNGEVALAIILKLYRACK 185

QY 165 -----LDIILQWMEETE 176

Db 186 NDYHELDLILKELMADTD 204

QY 186 NDYHELDLILKELMADTD 204

Db 186 NDYHELDLILKELMADTD 204

QY 186 NDYHELDLILKELMADTD 204

Db 186 NDYHELDLILKELMADTD 204

QY 186 NDYHELDLILKELMADTD 204

Db 186 NDYHELDLILKELMADTD 204

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Db 186 NDYHELDLILKELMADTD 204

QY 186 NDYHELDLILKELMADTD 204

Db 186 NDYHELDLILKELMADTD 204

QY 186 NDYHELDLILKELMADTD 204

```

QY 29 NGSCTVIANLGEIRGFSIDINGSVQAKGNDIDRLR-----RTESLDPTKANRC 80
Db 176 NGAGCAVDSRLSQ-RNSNDHLPIVQELSMKSIIEPTIHPETAKHGAVIDEILKPSYC 234
QY 81 CL-LRHLLATLYD-----RVPKNYOTPD--HYTLRKISSLSANFLTKDRLCHAMTC 132
Db 235 ILAVDALFELFENBIITWGSRVFEKHKVPIITIEVL-RIPY----LTFKSLRPPHPIKTA 288
QY 133 HCGEAMKKYSQILSHFE 150
Db 289 H-----LHRLLSFE 298

```

```

RESULT 12
S46367
Protein kinase CDCT (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 27-Jan-1995 #sequence
C:Accession: S46367; T39888
R:Fankhauser, C.; Simanis, V.
EMBO J. 13, 3011-3019, 1994
A:Title: The cdc7 protein kinase is a dosage dependent regulator of septum formation in
A:Reference number: S46367; MUID:94313982; PMID:803497
A:Accession: S46367
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA

```

A:Cross-references: UNIPROT:P41892; UNIPARC:UPI00000127259; EMBL:X78799; NID:g521098; PIR:R00001; A:Experimental source: wildtype 972. h.munc
A:Note: mRNA sequencing was also done to confirm the intron borders
R,Sandérs, D., Harris, D., Wood, V., Rajandream, M.A., Barrell, B.G.
submitted to the EMBL Data Library, February 1999
A:Reference number: Z21860
A:Accession: J39888
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1062 <SAU>
A:Cross-references: UNIPARC:UPI00000127259; EMBL:AL055537; PIDN:CAB36886.1; GSFDB:GN00067
A:Experimental source: Strain 972h-, cosmid c21
A:Genetic(s):
A:Gene: CDC7, SPDB:SPBC21.06c
A:Map position: II, 2
A:Introns: 9/3; 54/3; 64/3; 86/2; 171/1; 325/1; 405/3; 427/1; 544/3; 589/3
A:Function:
A:Description: essential for septum formation and cell division
E:Keywords: ATP; cell division; phosphotransferase; protein kinase
E:7-259/Domain: protein kinase homology <KIN>
E:15-23/Region: protein kinase ATP-binding motif

| | | | | | |
|----|-----------------------|---|---------------|-------|----------------------------------|
| | Query March | 8.9% | Score 81; | DB 2; | Length 1062; |
| | Best Local Similarity | 30.2%; | Pred. No. 15; | | |
| | Matches | 32; | Conservative | 20; | Mismatches 44; Indels 10; Gaps 4 |
| Oy | 23 | TGLKTLNIGSCVIATNLQEIIRNG-PSDRGSGVQAKDGNIDIRILHRTESLQPTKANROC | 81 | | |
| | | : : : : : | : | : | : |
| Dd | 466 | TGLGLTVLNKCGSWNNENEDGEESDDIPDSLETMLENDIE---- <td>520</td> <td></td> <td></td> | 520 | | |
| Oy | 82 | LRLRHLLLYLDVFNGYOTPDHYTSLRKISLSLANSFLTIKKOURLCH | 127 | | |
| | | : : : : : | : | : | : |
| Dd | 521 | LISLSLGSRD--KNIGSKD-TTVSQIASIISEDLSKRREITIAQH | 562 | | |

RESULT 13
 T19925
 hypothetical protein C44C10.4 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T19925
 R:Cottage, A.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: Z19197
 A:Accession: T19925
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-542 <WtL>
A:Cis8- references: UNIPROT:Q18616; UNIPARC:UPI000017B837; EMBL:Z69787; PIDD:CAA93638
A:Experimental source: clone C4C10
C:Genetics:
A:Gene: CESP:C4C10.4
A:Map position: X
A:Introns: 66/3; 229/3; 309/1; 328/3; 398/3

```
Query Match      8.8%; Score 80; DB 2; Length 542;  
Best Local Similarity 23.2%; Pred. No. 8.5;  
Matches 29; Conservative 25; Mismatches 43; Indels 28; Gaps 4
```

| | QY | DB | QY | DB | QY | DB |
|--|--|---|--|--|---------------|---------------|
| | 39 LQEIIRNGESDIRGSVOAKDGNIDIRILRTSTSLQDTPEANRCCLLHRLLYLDLVFPKNY 98 | 212 IQETKEKFVAEQGLKNNAKNAKMPKLISRSYSAIPKQTPEPN-----FKNN 256 | 99 -----QTPDRY----TKRKISSLSLNSFLTIKKDL---RLCAAHNTCHGGEPAWKYSQI 145 | 257 AIVAPRPKHNYHDNLITVDKLNLSYNKEKTERRELLQFVANNPNNINIRSEEGPNIIARE 316 | 146 LSHPF 150 | 317 IDYTE 321 |

RESULT 14
ADJ3160
hypochlorous acid
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_rev11 11-Jan-2002 #text_change 03-Jul-2004
C:Accession: ADJ3160
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, E.; Giller, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClintock, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: ADJ3160
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <KOR>
A:Cross-references: UNIPROT:Q9WRF4; UNIPARC:UPI00000D146D; GB:AE008687; PIDD:AAI45698
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: glnP/glnQ
A:Genome: plasmid

| | | | | | | |
|----|--|--------|---------------|-------|-------------|----------|
| | Query Match | 8.4% | Score 76.5; | DB 2, | Length 502; | |
| | Best Local Similarity | 24.6%; | Pred. No. 17; | | | |
| | Matches | 42; | Mismatches | 37; | Indels | 69; Gaps |
| | | | | | | 10 |
| Qy | 10 LLSAAYLLMT-PTGTL-----KTLNLGS---CVIATNIOEIRNGFSIDRSGVOA----- | 55 | | | | |
| Dd | 206 LLAGVFTLIYVPLPIHVNAINDRILRIKORPSVITSGLEEV-----SELDGAARASGVAF | 261 | | | | |
| Qy | 56 KGGNIDRIILRTSLSD-----TKPANCRC-----LRLHL----- | 86 | | | | |
| Dd | 262 KGGLDVRRLGMAYGDSDLVKGVDSVSPRGSVTCIGPGSGSKSTLLGLINLRIVEPKSGD | 321 | | | | |
| Qy | 87 -----LRLYLDRVFKNQYT--PDHYTLRKISLANSFLTIKK | 121 | | | | |
| Dd | 322 ILIDGESILAMKEPTLRRRVGVNIQHPELPFDH-----TALLENMLSLIK | 366 | | | | |

RESULT 15
B90153
2-isopropylmalate synthase, probable (leuA-1) [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
;Accession: B90153

R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R. et al., R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to Genbank, April 2001

A:Description: *Sulfolobus solfataricus* complete genome.

A:Reference number: A99139

A:Accession: B90153

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-553 <KUR>

A:Cross-references: UNIPROT:Q980Z1; UNIPARC:UPI00006418D; GB:AE006641; NID:g13813259; F

C:Genetics:

A:Gene: leuA-1

C:Superfamily: 2-isopropylmalate synthase leuA

Query Match 8.4%; Score 76.5; DB 2; Length 553;

Best local Similarity 19.6%; Pred. No. 19;

Matches 39; Conservative 34; Mismatches 61; Indels 65; Gaps 8;

QY 24 GLKTLNLSGCVIATNLQEI RNGPSDIRGSVQA---KGNID-----IRLR 67

Db 232 GIHAHNDIGCAVANSIMAIKAGARHVGRTINGIGRTGNADLIQIIPTLIKWGLNALNG 291

QY 68 TESLOPTKXANRCC-----LRLRLRLYLDRVFKNYQTPDH----- 103

Db 292 QESLRRLREVSRIIVEIILGPPNPYQPYGDNAFAHAGVHDVAMKVPAYEHVDPSLV 351

QY 104 ----YTLRKISSIAN--SFL-----TIKDLRLCHAMTCHGGEAMKKYSQILSHPE 150

Db 352 GNDRKIVISBELSGTANLVSYLGGLGTAIVDKDERL-----KKALNKIKELARGV 401

QY 151 KLE--POAAVVKALGELDI 167

Db 402 SPDVGPASAILTLTKEINI 420

Search completed: December 24, 2005, 10:48:30
Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 24, 2005, 10:35:50 ; Search time 230 Seconds

(without alignments)
539.883 Million cell updates/sec

Title: US-10-789-129-2

Perfect score: 910
Sequence: 1 MKASSIAFSLSAFYLTMT.....AVVKALGELDILLQWMEETR 176

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt_05.80:*

1: UniProt_sprot:*

2: UniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------------|--------------------|
| 1 | 906 | 99.6 | 176 | 1 | IL20_HUMAN | O9NYI1 homo sapien |
| 2 | 672 | 73.8 | 176 | 1 | IL20_MOUSE | O9JFV9 mus musculu |
| 3 | 337.5 | 37.1 | 177 | 1 | IL19_HUMAN | O9UND0 homo sapien |
| 4 | 337.5 | 37.1 | 215 | 2 | O5VUT3_HUMAN | O5VUT3 homo sapien |
| 5 | 306 | 33.6 | 168 | 2 | O4LDR4_BRARE | O4LDR4 brachydanio |
| 6 | 281.5 | 30.9 | 176 | 1 | IL19_MOUSE | O8CJ70 mus musculu |
| 7 | 266.5 | 29.3 | 175 | 2 | O7SK60_TETNG | O7SK60 tetradon n |
| 8 | 222 | 24.4 | 220 | 2 | O925J3_MOUSE | O925J3 mus musculu |
| 9 | 220 | 24.2 | 181 | 2 | O925S4_MOUSE | O925S4 mus musculu |
| 10 | 217 | 23.8 | 206 | 1 | IL24_HUMAN | O13007 homo sapien |
| 11 | 217 | 23.8 | 207 | 2 | O53XZ7_HUMAN | O53XZ7 homo sapien |
| 12 | 191 | 21.0 | 183 | 1 | MOBS_RAT | O9J124 rattus norv |
| 13 | 187 | 20.5 | 183 | 2 | O9WVFB_RAT | O9WVFB rattus norv |
| 14 | 175.5 | 19.3 | 175 | 2 | O6A2H5_CHICK | O6A2H5 gallus gall |
| 15 | 175.5 | 19.3 | 175 | 2 | O6A2H4_CHICK | O6A2H4 gallus gall |
| 16 | 161.5 | 17.7 | 178 | 1 | IL10_MACNE | P51497 macaca neme |
| 17 | 161 | 17.7 | 177 | 2 | O80ZJ6_9GAMA | O80ZJ6 cercopithe |
| 18 | 157.5 | 17.3 | 178 | 1 | IL10_MACFA | P79338 macaca fasc |
| 19 | 157.5 | 17.3 | 178 | 1 | IL10_MACMU | P51496 macaca mula |
| 20 | 157.5 | 17.3 | 178 | 1 | IL10_PAPHA | O5GCV6 papio hamad |
| 21 | 157.5 | 17.3 | 180 | 2 | O7J3I1_CYPCA | O7J3I1 cyprinus ca |
| 22 | 156.5 | 17.2 | 160 | 2 | O7JUZ1_HUMAN | O7JUZ1 homo sapien |
| 23 | 156.5 | 17.2 | 178 | 1 | IL10_FELCA | P52301 felis silve |
| 24 | 156.5 | 17.2 | 178 | 1 | IL10_FELCA | P52301 felis silve |
| 25 | 156.5 | 17.2 | 178 | 1 | O6FGM4_HUMAN | O6FGM4 homo sapien |
| 26 | 155 | 17.0 | 170 | 2 | IL10_EBV | P03180 Epstein-bar |
| 27 | 155 | 17.0 | 170 | 2 | O777H2_9GAMA | O777H2 human herpe |
| 28 | 154.5 | 17.0 | 175 | 1 | IL10_FIG | O29055 sus scrofa |
| 29 | 153 | 16.8 | 178 | 1 | IL10_MERUN | P47965 meriones un |
| 30 | 153 | 16.8 | 178 | 1 | IL10_MERUN | P47965 meriones un |
| 31 | 151.5 | 16.6 | 179 | 1 | IL10_CEREL | P51746 cervus elap |

| | | | | | | |
|----|-------|------|-----|---|---------------|---------------------|
| 32 | 151 | 16.6 | 178 | 1 | IL10_RABIT | O9EJ44 oryctolagus |
| 33 | 147.5 | 16.2 | 178 | 2 | O9TVD3_RABIT | O9TVD3 oryctolagus |
| 34 | 147.5 | 16.2 | 179 | 1 | IL10H_EHVT | P66678 equine herp |
| 35 | 147.5 | 16.2 | 179 | 1 | IL10H_EHVT | P66677 equine herp |
| 36 | 147 | 16.2 | 178 | 1 | IL10_MOUSE | P18893 mus musculu |
| 37 | 145.5 | 15.9 | 178 | 2 | O6FGS9_HUMAN | O6FGS9 mus musculu |
| 38 | 144.5 | 15.9 | 160 | 2 | O923T1_SIGHI | O923T1 sigmodon hi |
| 39 | 144.5 | 15.9 | 174 | 1 | IL10_TRIUV | O97798 trichosurus |
| 40 | 144.5 | 15.9 | 178 | 1 | IL10_HORSE | O28374 equus cabal |
| 41 | 143.5 | 15.8 | 178 | 2 | O6VVT1_BOBBU | O6VVT1 bubalus bub |
| 42 | 143 | 15.7 | 171 | 2 | O9Q5L1_CHV12 | O9Q5L1 cercopithe |
| 43 | 142.5 | 15.7 | 178 | 1 | IL10_BOVIN | P43480 bos taurus |
| 44 | 142.5 | 15.7 | 178 | 2 | O8MKG9_SAISSC | O8MKG9 salmistr sci |
| 45 | 142 | 15.6 | 181 | 1 | IL10_CANFA | P48411 canis famli |

ALIGNMENTS

RESULT 1

| ID | IL20_HUMAN | STANDARD: | PRT: | 176 AA. |
|----|--|-----------|------|---------|
| AC | O9NYI1; O96QZ6; | | | |
| DT | 28-FEB-2003 (Rel. 41, Created) | | | |
| DT | 29-MAR-2004 (Rel. 43, Last sequence update) | | | |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | | |
| DE | Interleukin-20 precursor (IL-20) (Four alpha helix cytokine zcyto10). | | | |
| GN | Name=IL20; Synonyms=ZCYT010; ORFNames=UN0852/PRO1801; | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; | | | |
| OC | Homio. | | | |
| OX | NCBI_Taxid=9606; | | | |
| RN | NP_061111 | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | |
| RX | MEDLINE=21097717; PubMed=1163236; DOI=10.1016/S0092-8674(01)00187-8; | | | |
| RA | Blumberg H., Conklin D., Xu W.F., Grossmann A., Brenden T., | | | |
| RA | Carollo S., Eagan M., Foster D., Haldeman B.A., Haugen H., | | | |
| RA | Tejnek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J., | | | |
| RA | Frankard D., Sexson S., Sprecher C., Waggle K., West J., | | | |
| RA | Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A., | | | |
| RT | "Interleukin 20: discovery, receptor identification, and role in | | | |
| RT | epidermal function."; | | | |
| RL | Cell 104:9-19(2001). | | | |
| RN | [2] | | | |
| RP | NUCLEOTIDE SEQUENCE (GENOMIC DNA). | | | |
| RA | Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., | | | |
| RA | Nickerson D.A.; | | | |
| RT | "SeattlesNPs. NHLBI HL66682 program for genomic applications, UW- | | | |
| RT | PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu)."; | | | |
| RT | Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [3] | | | |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. | | | |
| RA | MEDLINE=2288796; PubMed=12975309; DOI=10.1101/gr.1293003; | | | |
| RA | Clark H.F., Garney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., | | | |
| RA | Chen J., Chow B., Chui C., Crowley C., Curriel B., Deuel B., Dowd P., | | | |
| RA | Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S., | | | |
| RA | Huang A., Kim H.S., Klimoweki L., Jin Y., Johnson S., Lee J., | | | |
| RA | Leung L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J., | | | |
| RA | Seestaght S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., | | | |
| RA | Vandlen R.L., Watanebe C., Wiand D., Woods K., Xie M.-H., | | | |
| RA | Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., | | | |
| RA | Wood W.L., Godowski P.J., Gray A.M.; | | | |
| RT | "The secreted protein discovery initiative (SPDI), a large-scale | | | |
| RT | effort to identify novel human secreted and transmembrane proteins: a | | | |
| RT | bioinformatics assessment."; | | | |
| RT | Genome Res. 13:2265-2270(2003). | | | |
| RN | [4] | | | |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. | | | |
| RA | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., | | | |
| RA | Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | |

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uediri T.B., Toohilyuk S., Carninci P., Prange C.,
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McManus P.J., McKernan K.J., Malek J.A., Gamarine P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.U.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL PLoS Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP PROTEIN SEQUENCE OF 25-39,
 RX PdbMed=15340161; DOI=10.1110/ps.04682504;
 RA *Yang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites";
 RL Protein Sci. 13:2819-2824(2004).
 CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
 CC psoriasis. Acts through STAT3.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed at very low levels in skin, trachea,
 CC and other tissues.
 CC -1- SIMILARITY: Belongs to the IL-10 family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; AF224266; AAF36679.1; -; mRNA.
 DR EMBL; AF402002; AAK84423.1; -; Genomic_DNA.
 DR EMBL; AY558320; AAO8686.1; -; mRNA.
 DR EMBL; BC069311; AAH69311.1; -; mRNA.
 DR EMBL; BC069364; AAH69364.1; -; mRNA.
 DR EMBL; BC069398; AAH69398.1; -; mRNA.
 DR EMBL; BC069425; AAH69425.1; -; mRNA.
 DR EMBL; BC069449; AAH69449.1; -; mRNA.
 DR EMBL; BC069487; AAH69487.1; -; mRNA.
 DR EMBL; BC069523; AAH69523.1; -; mRNA.
 DR EMBL; BC069559; AAH69559.1; -; mRNA.
 DR EMBL; BC074948; AAH74948.1; -; mRNA.
 DR EMBL; BC074949; AAH74949.1; -; mRNA.
 DR HSSP; Q9UHD0; INIF.
 DR Ensemble; ENSG00000162891; Homo sapiens.
 DR HGNC; HGNC:6002; IL20.
 DR MIM; 605619; -;
 DR GO; GO:0005576; C:extracellular region; TAS.
 DR GO; GO:0045517; F:interleukin-20 receptor binding; TAS.
 DR GO; GO:0030097; P:hemoepoleis; ISS.
 DR GO; GO:0045606; P:positive regulation of epidermal cell diffe. .; TAS.
 DR GO; GO:0045618; P:positive regulation of keratinocyte diffe. .; TAS.
 DR GO; GO:0042517; P:positive regulation of tyrosine phosphoryla. .; TAS.
 DR GO; GO:0050727; P:regulation of inflammatory response; TAS.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR012352; IL-10 add helix.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR ProDom; PD003687; Interleukin_10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 KW Cytokine; Direct protein sequencing; Signal.
 FT CHAIN 1 24
 FT DISULFID 25 176 Interleukin-20.
 FT DISULFID 33 126 Potential.
 FT DISULFID 80 132 Potential.
 FT DISULFID 81 134 Potential.

FT CONFLICT 48 48 E -> D (in Ref. 1).
 FT CONFLICT 126 126 C -> S (in Ref. 3).
 SQ SEQUENCE 176 AA; 20072 MW; 8385992500B6C447 CRC64;
 Query Match 99.6%; Score 906; DB 1; Length 176;
 Best local similarity 99.4%; Pred. No. 1.8e-80;
 Matches 175; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKASSIAFSLSAAFYLLTPTSGKTLNLGSCVATINLQETIRNFSPIRGSVQAKGNI 60
 DB 1 MKASSIAFSLSAAFYLLTPTSGKTLNLGSCVATINLQETIRNFSPIRGSVQAKGNI 60
 QY 61 DIRLRRTSLDPTKRNACCILRHILRYLDRVFENVQTPHYLRKISLANSFLTIK 120
 DB 61 DIRLRRTSLDPTKRNACCILRHILRYLDRVFENVQTPHYLRKISLANSFLTIK 120
 QY 121 KDLRLCHAMTCHCGEAMKKTYSQILSHPEKLEPQAAVKAAGELDILQMMETE 176
 DB 121 KDLRLCHAMTCHCGEAMKKTYSQILSHPEKLEPQAAVKAAGELDILQMMETE 176
 RESULT 2
 IL20 MOUSE STANDARD; PRT; 176 AA.
 ID IL20 MOUSE
 AC Q9UKT9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10).
 GN Name=IL20; Synonyms=Zcyto10;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=21097717; PubMed=11163236; DOI=10.1016/S0092-8674(01)00187-8;
 RA Blumberg H., Conklin D., Xu W.F., Grossmann A., Brendler T.,
 RA Carrollo S., Eagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
 RA Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
 RA Prunkard D., Sexson S., Sprecher C., Wagie K., West J.,
 RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandra Sekher Y.A.;
 RT "Interleukin 20: discovery, receptor identification, and role in
 RT epidermal function.";
 RL Cell 104:9-19(2001).
 CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
 CC psoriasis. Acts through STAT3.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-10 family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; AF224267; AAF36680.1; -; mRNA.
 DR HSSP; Q9UHD0; INIF.
 DR Ensemble; ENSMUSG0000026416; Mus musculus.
 DR MGI; MGI:1890473; IL20.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0045517; F:interleukin-20 receptor binding; IDA.
 DR GO; GO:0030097; P:hemoepoleis; NAS.
 DR GO; GO:0045606; P:positive regulation of epidermal cell diffe. .; ISS.
 DR GO; GO:0045618; P:positive regulation of keratinocyte diffe. .; ISS.
 DR GO; GO:0042517; P:positive regulation of tyrosine phosphoryla. .; ISS.
 DR GO; GO:0050727; P:regulation of inflammatory response; ISS.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR ProDom; PD003687; Interleukin_10; 1.


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DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 176 Interleukin-20.
FT DISULFID 33 126 Potential.
FT DISULFID 80 132 Potential.
FT DISULFID 81 134 Potential.
SQ SEQUENCE 176 AA; 20098 MW; 08577AF656574771 CRC64;

Query Match
Best Local Similarity 73.8%; Score 672; DB 1; Length 176;
Matches 131; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 MKASLSAFSLISAFYLTWPTSTGLTNLNGSCVIAITNLOEIRNGFSIDRIGSVQAKDNI 60
DB 1 MKGFGIAFLGFSVGLWLTPLTGLTTHLHSGCVITANLQAIQKSESLRDSVQAEYDNI 60
QY 61 DIRILARTESLODTPKANRCCLRLRLRLYLDRVFNKYOTPDHYTLRKISLSLNSFLITK 120
DB 61 DIRILARTESLODTPKANRCCLRLRLRLYLDRVFNKYOTPDHYTLRKISLSLNSFLITK 120
QY 121 KDLRLCHAMTTCGCEGSEAKKYSQIISHEKLEPQAAVYKALGELDILIQMEE 174
DB 121 KDLVCHSHMACGCEGSEAMEKYNQIISHFTELELQAAVYKALGELDILIRMEE 174

RESULT 3
IL19_HUMAN STANDARD; PRT; 177 AA.
ID IL19_HUMAN
AC Q9UHD0; Q96QR4; Q9NUV0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-19 precursor (IL-19) [Melanoma differentiation associated
DE protein-1-like protein] (NG.1).
GN Name=IL19; Synonyms=ZMDA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21040165; PubMed=1196675; DOI=10.1038/sj.gene.6363714;
RA Gallagher G., Dickenheets H., Eskdale J., Iotova L.S.,
RA Mitrochukchenko O.V., Peat J.D., Vasquez S., Donnelly R.P.,
RA Kotenko S.V.;
RA "Cloning, expression and initial characterization of interleukin-19
RA (IL-19), a novel homolog of human interleukin-10 (IL-10).";
RL Genes Immun. 1:442-450(2000).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22257669; PubMed=12370360;
RA Liao Y.-C., Liang W.G., Chen F.W., Hsu J.H., Yang J.J., Chang M.-S.;
RA "IL-19 induces production of IL-6 and TNF-alpha and results in cell
RA apoptosis through TNF-alpha.";
RL J. Immunol. 169:4288-4297(2002).
RN (3)
RP NUCLEOTIDE SEQUENCE.
RA Conklin D., Petersen J., Loften-Day C., Whitmore T., Muerer M.,
RA Sexson S., Smith D., Lok S., Powder T., O'Hara P.;
RA "Homo sapiens homolog of melanoma differentiation associated gene.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN (4)
RP NUCLEOTIDE SEQUENCE.
RA Kotenko S.V., Pestka S.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN (5)
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] AND VARIANT PHE-175.
RA Rieder M.U., Carrington D.P., Chung W.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RA "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
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RT FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN (6)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN (7)
RP PROTEIN SEQUENCE OF 25-39.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN (8)
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 19-177, AND DISULFIDE BONDS.
RX PubMed=12403790; DOI=10.1074/jbc.M208602200;
RA Chang C., Magracheva E., Kozlov S., Fong S., Tobin G., Kotenko S.,
RA Wlodawer A., Zdanov A.;
RT "Crystal structure of interleukin-19 defines a new subfamily of
RT helical cytokines.";
RL J. Biol. Chem. 278:3308-3313(2003).
CC -1- FUNCTION: May play some important roles in inflammatory responses.
CC -1- UP-regulates IL-6 and TNF-alpha and induces apoptosis (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF276915; AAG16755.1; -; Genomic_DNA.
CC EMBL; AF453946; AAN40906.1; -; mRNA.
CC EMBL; AF192498; AAF06663.1; -; mRNA.
CC EMBL; AY040367; AAK91776.1; ALT INIT; mRNA.
CC EMBL; AF390905; AAK64498.1; -; Genomic_DNA.
CC EMBL; AL049615; CAB72342.1; -; Genomic_DNA.
CC PDB; 1N1F; X-ray; A=19-177.
CC DR Ensembl; ENSG00000142224; Homo sapiens.
CC DR HGNC; HGNC:5990; IL19.
CC DR MIM; 605687; -.
CC DR GO; GO:0005576; C:extracellular region; NAS.
CC DR GO; GO:0005125; P:cytokine activity; TAS.
CC DR GO; GO:0006935; P:immune response; NAS.
CC DR GO; GO:0007165; P:signal transduction; NAS.
CC DR InterPro; IPR012351; Cytokine 4 hlx.
CC DR InterPro; IPR000098; Interleukin_10.
CC DR Pfam; PF00726; IL10; 1.
CC DR SMART; SM00188; IL10; 1.
CC DR PROSITE; PS00520; INTERLEUKIN_10; 1.
CC KW 3D-structure; Apoptosis; Cytokine; Direct protein sequencing;
CC KW Glycoprotein; Polymorphism; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 177 Interleukin-19.
CC FT CARBOHD 56 56 N-linked (GlcNAc...) (potential).
CC FT CARBOHD 135 135 N-linked (GlcNAc...) (potential).
CC FT DISULFID 28 121
CC FT DISULFID 75 127
CC FT DISULFID 76 129
CC FT VARIANT 175 175 S -> F.
CC FT SEQUENCE 177 AA; 20392 MW; 7CCFAC22177DB408 CRC64;

Query Match
Best Local Similarity 37.1%; Score 337.5; DB 1; Length 177;
Matches 69; Conservative 36; Mismatches 64; Indels 5; Gaps 1;

QY 1 MKASLSAFSLISAFYLTWPTSTGLTNLNGSCVIAITNLOEIRNGFSIDRIGSVQAKDNI 60
DB 1 MKLQCVSLMLGLTILILCSVDNHGR-----RCLISTDMHHIEESFOIKRAIOAKDTFP 55
```

QY 61 DIRILARTESLODKTPANRCCILRLHLRLYLDRVPKRYQTPDHTYTKISSIANSPLTTK 120
 DB 56 NVTILSTLETLQIKPLDVCCVTKNLAFAVDVFQKHOPNPKIRKISSIANSFLYMQ 115
 QY 121 KDIRLCHAHMTCCGSEAMKKYSQILSHFEKLEPOAAVVAALGELDILQWME 174
 DB 116 KTRROCOBQRCRQCRQATNATRYIHNDYQLEVHAHAATSLGELDFLAMINK 169

RESULT 4
 OSUT3 HUMAN
 ID OSUT3_HUMAN PRELIMINARY; PRT; 215 AA.

AC OSUT3;
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Interleukin 19.
 GN Name=IL19; ORFNames=RP11-262N9.2-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kay M.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL; AL513315; CAH71814.1; -; Genomic DNA.
 DR SMR; OSUT3; 60-215.
 DR Ensembl; ENSG00000142224; Homo sapiens.
 DR GO; GO:0005615; C:extracellular space; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; UNKNOWN_1.
 DR Cytokine.
 KW CYTOKINE.
 SQ SEQUENCE 215 AA; 24567 MW; D79DB0F11DA74B4 CRC64;

Query Match 37.1%; Score 337.5; DB 2; Length 215;
 Best Local Similarity 39.7%; Pred. No. 1.2e-24;
 Matches 69; Conservative 36; Mismatches 64; Indels 5; Gaps 1;
 QY 1 MKASIAFSLISAAYLLWTPSTGLKTLNLSGVATNLQEIRNGFSDIRGSVOAKDGT 60
 DB 39 MKLQCVSLWLGITLILCSVDNGLR-----RGLSTDMHIEESFQEIKRAIQAKTFP 93
 QY 61 DIRILARTESLODKTPANRCCILRLHLRLYLDRVPKRYQTPDHTYTKISSIANSPLTTK 120
 DB 94 NVTILSTLETLQIKPLDVCCVTKNLAFAVDVFQKHOPNPKIRKISSIANSFLYMQ 153
 QY 121 KDIRLCHAHMTCCGSEAMKKYSQILSHFEKLEPOAAVVAALGELDILQWME 174
 DB 154 KTRROCOBQRCRQCRQATNATRYIHNDYQLEVHAHAATSLGELDFLAMINK 207

RESULT 5
 Q4UDR4 BRARE
 ID Q4UDR4_BRARE PRELIMINARY; PRT; 168 AA.
 AC Q4UDR4;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Interleukin 10 family protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ram S.; Daisuke I.; Sakai M.;

RT "Evolution of IL-10 family genes in teleosts."
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB219579; BAE06181.1; -; mRNA.
 SQ SEQUENCE 168 AA; 19110 MW; 807D18AD736C709B CRC64;

Query Match 33.6%; Score 306; DB 2; Length 168;
 Best Local Similarity 42.4%; Pred. No. 1.1e-21;
 Matches 67; Conservative 27; Mismatches 58; Indels 6; Gaps 3;
 QY 18 LWTPTGTLNLSGVATNLQEIRNGFSDIRGSVOAKDGTDIRLR--TESLODK 75
 DB 10 LWDAAQG-RRLHSGCKVNIHTHELRRHFQYRGWISGDDKGRRLAKDWNLSQATE 68
 QY 76 PANRCCILRLHLRLYLDRVPKRYQTPDHTYTKISSIANSPLTTKDIRLCHAHMTCCG 135
 DB 69 ---SCCFLEQLLHFYMDVFFISYSSHSIHRRTTSTLANSPLISDKLRCVCHANACECG 125
 QY 136 EAMKKYSQILSHFEKLEPOAAVVAALGELDILQWME 173
 DB 126 ENTRLQKSIQRYVEKLDQAAGTVKALGELDSLLEWIE 163

RESULT 6
 IL19 MOUSE
 ID IL19_MOUSE STANDARD; PRT; 176 AA.
 AC Q8CJ70;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-19 precursor (IL-19).
 GN Name=IL19;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND FUNCTION.
 RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=22257669; PubMed=12370360;
 RL Liao Y.-C., Liang W.-G., Chen F.-W., Hsu J.-H., Yang J.-J., Chang M.-S.,
 RT "IL-19 induces production of IL-6 and TNF-alpha and results in cell
 apoptosis through TNF-alpha."
 RL J. Immunol. 169:4288-4297(2002).
 CC -1- FUNCTION: May play some important roles in inflammatory responses.
 CC up-regulates IL-6 and TNF-alpha and induces apoptosis.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-10 family.
 CC -----
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 CC -----
 CC EMBL; AF453945; AAN40905.1; -; mRNA.
 DR HSSP; Q9UHD0; INF.
 DR SMR; Q8CJ70; 23-170.
 DR Ensembl; ENSMUSG0000016524; Mus musculus.
 DR MGI; MGI:1890472; IL19.
 DR GO; GO:0006917; P:induction of apoptosis; IDA.
 DR GO; GO:0042226; P:interleukin-6 biosynthesis; IDA.
 DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000098; Interleukin_10.
 DR Prodom; PD003687; Interleukin_10; 1.
 DR SWART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; FALSE NEG.
 KW Apoptosis; Cytokine; Glycoprotein; Signal.
 DR Apoptosis; PS00520; INTERLEUKIN_10; FALSE NEG.
 KW Apoptosis; Cytokine; Glycoprotein; Signal.
 FT CHAIN 1
 FT SIGNAL 24
 FT STANAL 25
 FT CARBOHYD 56
 FT CARBOHYD 127
 FT CARBOHYD 127
 FT N-linked (GlcNAc...) (Potential).
 FT N-linked (GlcNAc...) (Potential).

FT CARBOHYD 134 134 N-linked (GlcNAc...) (Potential).
 FT DISULFID 28 120 By similarity.
 FT DISULFID 74 126 By similarity.
 FT DISULFID 75 128 By similarity.
 SQ SEQUENCE 176 AA; 20288 MW; 7386C1BC54077FDC CRC64;

Query Match 30.9%; Score 281.5; DB 1; Length 176;
 Best Local Similarity 38.6%; Pred. No. 2.9e-19;
 Matches 56; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

QY 29 NUGSCYATNLOEIRNGFSDIRGSVQAKGNDIRILRRTESIQDTKPNRCCLLHRLR 88
 DB 24 SLRRCISIVDMRIEKSFKHKKAMQTKTFKKNVTL-SLENLRISIKPGVCCMTNNLLT 82
 QY 89 LVLDKRVKQVQTPDHYTLTKRISLSANSPITIKDILCHAHMTCHGGEAMKKYSQILSH 148
 DB 83 FTRDRVFQDHQERSLEVLNRISISANSPITIKDILCHAHMTCHGGEAMKKYSQILSH 142
 QY 149 PERLEPOAAVVKALGELDILLQWME 173
 DB 143 YNQLSVSAALSKSLGELNILLAMID 167

RESULT 7
 ID Q7SX60_TETNG PRELIMINARY; PRT; 175 AA.
 AC Q7SX60_

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Interleukin-20.
 GN Name=IL20;
 OS Tetradodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontinae; Tetraodon.
 NC NCB1_Taxid=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=12869211; DOI=10.1186/1471-2164-4-29;
 RA Lutfalla G., Crolius H.R., Stange-Thomann N., Jallion O.,
 RA Mogensson K., Monneron D.;
 RT "Comparative genomic analysis reveals independent expansion of a
 RT lineage-specific gene family in vertebrates: The class II cytokine
 RT receptors and their ligands in mammals and fish.";
 RL BMC Genomics 4:29-29(2003).
 DR EMBL; AY294557; AAP57414.1; -; Genomic_DNA.
 DR EMBL; AY294558; AAP57416.1; -; mRNA.
 DR GO; GO:0005615; C:extracellular space; IEA.
 DR GO; GO:0005125; P:immune response; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR000098; Interleukin_10.
 DR Pfam; PF00726; IL10; 1.
 DR Prodom; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 SQ SEQUENCE 175 AA; 19838 MW; DE6FA67E0038E034 CRC64;

Query Match 29.3%; Score 266.5; DB 2; Length 175;
 Best Local Similarity 38.0%; Pred. No. 8.4e-18;
 Matches 57; Conservative 33; Mismatches 53; Indels 7; Gaps 3;

QY 26 KTLNAGSCYATNLOEIRNGFSDIRGSVQAKGNDIRILRRTESIQDTKPNRCCLLHRLR 85
 DB 24 QTLNAGSCISADLQEMQHSHNRINATLDEBEIGVKLSK-RLMEDVDQDRCCTFLRL 82
 QY 86 LRLVLDKRVKQVQTPDHYTLTKRISLSANSPITIKDILCHAHMTCHGGEAMKKYS 143
 DB 83 VLQFIIDKVFPSYLSHPNQGSSSSSLANTFTIIRKQMTQKCH-----CLCQETQKQVD 138
 QY 144 QILSHFEKLEPOAAVVKALGELDILLQWME 173

DB 139 SILDAFNKLEASKAVLKAVGELDTVLQWIQ 168

RESULT 8
 ID Q925J3_MOUSE PRELIMINARY; PRT; 220 AA.
 AC Q925J3_

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Th2-specific cytokine FISP.
 GN Name=IL24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NC NCB1_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;
 RX MEDLINE=21240641; PubMed=11342597;
 RA Schaefer G., Venkataraman C., Schindler U.,
 RT "FISP (IL-4-induced secreted protein), a novel cytokine-like molecule
 RT secreted by Th2 cells.";
 RL J. Immunol. 166:5859-5863(2001).
 CC -1-SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL; AF333251; AAK52470.1; -; mRNA.
 DR Ensembl; ENSMUSG0000026420; Mus musculus.
 DR MGI; MGI:213548; IL24.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR000098; Interleukin_10.
 DR Prodom; PD003687; Interleukin_10; 1.
 DR SMART; SM00188; IL10; 1.
 DR PROSITE; PS00520; INTERLEUKIN_10; 1.
 KW Cytokine.
 SQ SEQUENCE 220 AA; 25168 MW; 5BF76C8612AC909D CRC64;

Query Match 24.4%; Score 222; DB 2; Length 220;
 Best Local Similarity 34.4%; Pred. No. 2.6e-13;
 Matches 56; Conservative 30; Mismatches 71; Indels 6; Gaps 4;

QY 17 LLMTSTGTL-KTLNAGSC-VIATNLOEIRNGFSDIRGSVQAKGNDIRILRRTESIQDT 73
 DB 55 LLMNGVPLGEQGEFFGSCQVTVGLPELMEFRTVKNVTVQDQDITSRLL-KQVLRN 113
 QY 74 TKPNRCCILRLRLVLDKRVKQVQTPDHYTLTKRISLSANSPITIKDILCHAHMT 131
 DB 114 VSGAGSCYLAHSLKFLNTVFKNHSKIAKPKVLRSESTLANNFIVIMSGLOPKDSNM 173
 QY 132 CHGGEAMKKYSQILSHFEKLEPOAAVVKALGELDILLQWME 174
 DB 174 LPISSEAHQRFLLFRARQDLTEVALVKAEGEVDILLTMQK 216

RESULT 9
 ID Q925S4_MOUSE PRELIMINARY; PRT; 181 AA.
 AC Q925S4_

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Melanoma differentiation associated gene-7.

GN Name=IL24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NC NCB1_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SvJ;
 RA Madiredi M.T., Lin J., Su Z., Shay J.W., Huberman E., Fisher P.B.,
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.


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FT SIGNAL 1 51 Interleukin-24.
FT CHAIN 52 206 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 85 206 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 99 99 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 126 126 N-linked (GlcNAc... ) (Potential).
FT VARIANT 124 124 Y -> H (in dSNP:1150258) .
FT VARIANT 125 125 /FtId=VAR_011974.
FT VARIANT 125 125 H -> R (in dSNP:3093431) .
FT VARIANT 131 131 /FtId=VAR_013097.
FT VARIANT 131 131 V -> L (in dSNP:3093446) .
FT VARIANT 131 131 /FtId=VAR_013098.
FT VARIANT 131 131 A -> AS (in Ref. 4) .
FT CONFLICT 14 14
FT SEQUENCE 206 AA; 23825 MW; CB8135083EAB8DD CRC64;

Query Match 23.8%; Score 217; DB 1; Length 206;
Best Local Similarity 32.8%; Pred. No. 7.3e-13;
Matches 57; Conservative 39; Mismatches 66; Indels 12; Gaps 5;

QY 6 LAFSLISAAPFYLLMPTSTGL--KTLNLGSCVIATNL-QEIRNGFSDIRGSVOAKDGNIDI 62
DB 37 LGFTL-----LLMSQVSGAGQGEFFHGPQVKGVPQKMEAFVAKDTMOAQDNITSA 90

QY 63 RIIRRTESLODTPARPCCLRLHLVLDVRKNT--QTPDHYTKRISLSLANSFLTK 120
DB 91 RLKQO-EVLQNVSDAESCYLEVHTLEFYLKTVFKYHNHRTVEVRLTKSFSTLANNFVLIV 149

QY 121 KDLRLCHAMTCHGCEAMKKYSQILSHPEKLEPQAAVYKALGELDILLQWMBE 174
DB 149 SOLQPSQENEMFSIRDSARRRLLFRARFKQDVEALTKALGCEVDILLTMQK 202

RESULT 11
053X27 HUMAN PRELIMINARY; PRT; 207 AA.
AC 053X27;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Interleukin 24.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kaimine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Pheasant M., Farmer A.
RT Cloning of human full-length cDS in BD Creator(TM) system donor
RT vector.
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC EMBL; BT007156; AAP35820.1; -; mRNA.
DR GO; GO:0005576; Cytoplasmic region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
KW Cytokine.
SQ SEQUENCE 207 AA; 23912 MW; 17687A467B9CB551 CRC64;

Query Match 23.8%; Score 217; DB 2; Length 207;
Best Local Similarity 32.8%; Pred. No. 7.4e-13;
Matches 57; Conservative 39; Mismatches 66; Indels 12; Gaps 5;

QY 6 LAFSLISAAPFYLLMPTSTGL--KTLNLGSCVIATNL-QEIRNGFSDIRGSVOAKDGNIDI 62
DB 37 LGFTL-----LLMSQVSGAGQGEFFHGPQVKGVPQKMEAFVAKDTMOAQDNITSA 90

QY 63 RIIRRTESLODTPARPCCLRLHLVLDVRKNT--QTPDHYTKRISLSLANSFLTK 120
DB 91 RLKQO-EVLQNVSDAESCYLEVHTLEFYLKTVFKYHNHRTVEVRLTKSFSTLANNFVLIV 149

QY 121 KDLRLCHAMTCHGCEAMKKYSQILSHPEKLEPQAAVYKALGELDILLQWMBE 174
DB 149 SOLQPSQENEMFSIRDSARRRLLFRARFKQDVEALTKALGCEVDILLTMQK 202

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DB 150 SOLQPSQENEMFSIRDSARRRLLFRARFKQDVEALTKALGCEVDILLTMQK 203

RESULT 12
MOB5 RAT STANDARD; PRT; 183 AA.
ID MOB5 RAT
AC 09U124;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cytokine-like protein Mob-5 precursor.
GN Name=MOB5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20387329; PubMed=10825166; DOI=10.1074/jbc.M001958200;
RA Zhang R., Tan Z., Liang P.,
RT Identification of a novel ligand-receptor pair constitutively
RT activated by ras oncogenes.
RL J. Biol. Chem. 275:24436-24443(2000).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF269251; AAF75553.1; -; mRNA.
CC Ensemble; ENSRN00000004470; Rattus norvegicus.
DR GO; GO:0048144; P:fibroblast proliferation; TAS.
DR GO; GO:0042060; P:wound healing; TAS.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR000098; Interleukin_10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00186; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 183 Cytokine-like protein Mob-5.
FT CARBOHYD 76 76 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 183 AA; 21096 MW; AFA11446C491AC4 CRC64;

Query Match 21.0%; Score 191; DB 1; Length 183;
Best Local Similarity 33.1%; Pred. No. 2.2e-10;
Matches 49; Conservative 31; Mismatches 60; Indels 8; Gaps 5;

QY 31 GSC-VIATNLQEIRNGFSDIRGSVOAKDGNIDIRIRRTESLODTPARPCCLRLHLRL 89
DB 34 GCGQVTGVLPRLEMAFWVTKVTKQDELSVRL-KPQVLQNVSDAESCYLEVHTLEF 92

QY 90 YLDVRPKNYQTP-DHYTKRISLSLANSFLTKDRLCHAMTCHGCEAMKKYSQILS 147
DB 93 YLNTVFKNYHRSKIVFKVLYKSFSTLANNFVIMSKLQPSKDNAMPISDARRF--ILY 150

QY 148 H--FEKLEPQAAVYKALGELDILLQWMBE 173
DB 151 HRTFKQDLEVALARAFSGVDILLAMQ 178

RESULT 13
09WVP8 RAT PRELIMINARY; PRT; 183 AA.
ID 09WVP8 RAT
AC 09WVP8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

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DE C49a.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=99308986; PubMed=10381256;
RX DOI=10.1002/(SICI)1097-4644(19990701)74:1<1::AID-JCB1>3.0.CO;2-D;
RA Soo C., Shaw W.W., Freymiller E., Longaker M.T., Bertolami C.N.,
RA Chiu R., Tieu A., Ting K.,
RT "Cutaneous rat wounds express c49a, a novel gene with homology to the
RT human melanoma differentiation associated gene, mda-7.",
RL J. Cell. Biochem. 74:1-10(1999).
CC -1. SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL: AF004774; AAB69171.1; -; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR000098; Interleukin_10.
DR ProDom: PD003687; Interleukin_10.
DR PROSITE: PS00520; INTERLEUKIN_10; 1.
KM Cytokine.
SQ SEQUENCE 183 AA; 21052 MW; FF69A96AF473E4F CRC64;

Query Match 20.5%; Score 187; DB 2; Length 183;
Best Local Similarity 32.2%; Pred. No. 5.5e-10;
Matches 47; Conservative 29; Mismatches 66; Indels 4; Gaps 3;

QY 31 GGC-VIATNLQEIIRNGFSIRSVQAKGNIDIRILRRTSLDDTPANECCLRLHLRL 89
DB 34 GPCQVGVGVPELMEAFWTKVNTKTDLTSLARLL-KPQVLQNVSPAESCYLAHSLK 92
QY 90 YLDRVFNKYQTP--DHTLTKRISLANSFLTKKDLRLGHAHTCHGGEAMKKYSQILS 147
DB 93 YLNTVFKNYHSHKVKRFKVLVSFSTLANFLVMSKLOPSKONMLPLISARRRFLFLFR 152
QY 148 HPEKLEPOAAVVRALGELDILLQWME 173
DB 153 TFKQDIEVALAKAFGEVDILLMMQ 178

RESULT 14
O6A2H5 CHICK PRELIMINARY; PRT; 175 AA.
ID O6A2H5_
AC 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Interleukin-10.
GN Name=IL-10;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC Rothenwell L., Young J., Zoarob R., Whitaker C.A., Heeketh P.,
RA Archer A., Smith A.L., Kaiser P.,
RT "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT Immune Response to Eimeria maxima.",
RL J. Immunol. 173:2675-2682(2004).
DR EMBL: AJ621254; CAP18432.1; -; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR012351; Cytokine 4 hlx.
DR InterPro: IPR012352; IL-10 add helix.
DR InterPro: IPR000098; Interleukin_10.
DR Pfam: PF00726; IL10; 1.

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DR PRINTS: PR01294; INTERLEUKIN10.
DR ProDom: PD003687; Interleukin_10; 1.
DR SMART: SM00188; IL10; 1.
SQ SEQUENCE 175 AA; 20514 MW; B0966EBEADF050 CRC64;

Query Match 19.3%; Score 175.5; DB 2; Length 175;
Best Local Similarity 30.3%; Pred. No. 7e-09;
Matches 53; Conservative 32; Mismatches 81; Indels 9; Gaps 5;

QY 1 MKASSLAFSLLSAFLYLTWPTSGTKTLNLG-SCVIATNLQEIIRNGFSIRSVQAKDGN 59
DB 1 MTCGCCALLLLLAACLT---PAHCLPPTCLHFSLELPARLRVRFEEIKDYFGQRDDE 57
QY 60 IDIRILRRTESLDDTPANRCCILRLHLLYLDRVPKNTQTDHYTLRKISSLANSFLTL 119
DB 58 LNIQLL-SESLDEFKGTGCGSVSEMLRFYDDEVLPARAMQSTSHQSGMDGNLGL 116
QY 120 KQDLRLCHAHMTCHGGEAMKKYSQILSHPEKLEPOAAVVRALGELDILLQWME 174
DB 117 KATMRCHRFPTC---EKRSKAIKQIKETFEKMD-ENGIIYKAMGEFDIFINYLEE 167

RESULT 15
O6A2H4 CHICK PRELIMINARY; PRT; 175 AA.
ID O6A2H4_
AC 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Interleukin-10.
GN Name=IL10;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC Rothenwell L., Young J., Zoarob R., Whitaker C.A., Heeketh P.,
RA Archer A., Smith A.L., Kaiser P.,
RT "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT Immune Response to Eimeria maxima.",
RL J. Immunol. 173:2675-2682(2004).
DR EMBL: AJ621254; CAP21727.1; -; Genomic DNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR012351; Cytokine 4 hlx.
DR InterPro: IPR012352; IL-10 add helix.
DR InterPro: IPR000098; Interleukin_10.
DR Pfam: PF00726; IL10; 1.
DR PRINTS: PR01294; INTERLEUKIN10.
DR ProDom: PD003687; Interleukin_10; 1.
DR SMART: SM00188; IL10; 1.
SQ SEQUENCE 175 AA; 20496 MW; A4966ABAAPDFB057 CRC64;

Query Match 19.3%; Score 175.5; DB 2; Length 175;
Best Local Similarity 30.3%; Pred. No. 7e-09;
Matches 53; Conservative 32; Mismatches 81; Indels 9; Gaps 5;

QY 1 MKASSLAFSLLSAFLYLTWPTSGTKTLNLG-SCVIATNLQEIIRNGFSIRSVQAKDGN 59
DB 1 MTCGCCALLLLLAACLT---PAHCLPPTCLHFSLELPARLRVRFEEIKDYFGQRDDE 57
QY 60 IDIRILRRTESLDDTPANRCCILRLHLLYLDRVPKNTQTDHYTLRKISSLANSFLTL 119
DB 58 LNIQLL-SESLDEFKGTGCGSVSEMLRFYDDEVLPARAMQSTSHQSGMDGNLGL 116
QY 120 KQDLRLCHAHMTCHGGEAMKKYSQILSHPEKLEPOAAVVRALGELDILLQWME 174
DB 117 KATMRCHRFPTC---EKRSKAIKQIKETFEKMD-ENGIIYKAMGEFDIFINYLEE 167

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Tue Jan 3 11:53:21 2006

us-10-789-129-2.rup

Page 9

Search completed: December 24, 2005, 10:46:54
Job time : 230 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 28, 2005, 13:49:18 / Search time 2943 Seconds

(without alignments)
2781.331 Million cell updates/sec

Title: US-10-789-129-26

Perfect score: 753
Sequence: 1 CVIATNLOEIRNGFSDIRG.....AVKALGHEIDILLQWMEETE 144

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+.p2n.model -DEV=rlp
-O=/gen2.1/USFTO_spool_p/US10789129/runat_23122005_152720_20263/app_query.fasta_1.327
-DB=genemb1 -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10789129 @CGN 1.1 7415 @runat_23122005_152720_20263 -NCPU=6 -ICPU=3
-NO WMAP -LANG=QUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmb1:
1: gb_da:
2: gb_in:
3: gb_env:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pr:
9: gb_ro:
10: gb_sts:
11: gb_sy:
12: gb_un:
13: gb_vl:
14: gb_hlg:
15: gb_pl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 753 | 100.0 | 926 | 6 | BD087297 Mammalian |
| 2 | 753 | 100.0 | 926 | 6 | CQ818183 Sequence |
| 3 | 753 | 100.0 | 926 | 6 | CS109174 Sequence |

| | | | | | | |
|----|-------|-------|------|----|----------|--------------------|
| 4 | 753 | 100.0 | 926 | 6 | CS110179 | CS110179 Sequence |
| 5 | 753 | 100.0 | 926 | 6 | AR342856 | AR342856 Sequence |
| 6 | 753 | 100.0 | 926 | 6 | AP242866 | AP242866 Homo sapi |
| 7 | 749 | 99.5 | 462 | 6 | CS123418 | CS123418 Sequence |
| 8 | 749 | 99.5 | 531 | 8 | BC069311 | BC069311 Homo sapi |
| 9 | 749 | 99.5 | 531 | 8 | BC069364 | BC069364 Homo sapi |
| 10 | 749 | 99.5 | 531 | 8 | BC069398 | BC069398 Homo sapi |
| 11 | 749 | 99.5 | 531 | 8 | BC069425 | BC069425 Homo sapi |
| 12 | 749 | 99.5 | 531 | 8 | BC069449 | BC069449 Homo sapi |
| 13 | 749 | 99.5 | 531 | 8 | BC069487 | BC069487 Homo sapi |
| 14 | 749 | 99.5 | 531 | 8 | BC069523 | BC069523 Homo sapi |
| 15 | 749 | 99.5 | 531 | 8 | BC069559 | BC069559 Homo sapi |
| 16 | 749 | 99.5 | 531 | 11 | AY888562 | AY888562 Synthetic |
| 17 | 749 | 99.5 | 531 | 11 | AY891211 | AY891211 Synthetic |
| 18 | 749 | 99.5 | 531 | 11 | AY893295 | AY893295 Synthetic |
| 19 | 749 | 99.5 | 603 | 8 | BC074948 | BC074948 Homo sapi |
| 20 | 749 | 99.5 | 603 | 8 | BC074949 | BC074949 Homo sapi |
| 21 | 749 | 99.5 | 867 | 6 | AX498605 | AX498605 Sequence |
| 22 | 749 | 99.5 | 867 | 6 | AX537938 | AX537938 Sequence |
| 23 | 746 | 99.1 | 926 | 6 | CQ889881 | CQ889881 Sequence |
| 24 | 746 | 99.1 | 926 | 6 | CQ889943 | CQ889943 Sequence |
| 25 | 739 | 98.1 | 1571 | 6 | CQ970652 | CQ970652 Sequence |
| 26 | 739 | 98.1 | 1571 | 6 | CS133455 | CS133455 Sequence |
| 27 | 739 | 98.1 | 1571 | 6 | AX092406 | AX092406 Sequence |
| 28 | 739 | 98.1 | 1571 | 6 | AX358964 | AX358964 Sequence |
| 29 | 739 | 98.1 | 1571 | 6 | AX362457 | AX362457 Sequence |
| 30 | 739 | 98.1 | 1571 | 6 | AX376542 | AX376542 Sequence |
| 31 | 739 | 98.1 | 1571 | 6 | AX454700 | AX454700 Sequence |
| 32 | 739 | 98.1 | 1571 | 6 | AX463964 | AX463964 Sequence |
| 33 | 739 | 98.1 | 1571 | 6 | AX464412 | AX464412 Sequence |
| 34 | 739 | 98.1 | 1571 | 6 | AX491178 | AX491178 Sequence |
| 35 | 739 | 98.1 | 1571 | 6 | AX697333 | AX697333 Sequence |
| 36 | 739 | 98.1 | 1571 | 8 | AY358320 | AY358320 Homo sapi |
| 37 | 686 | 91.1 | 747 | 6 | BD087304 | BD087304 Mammalian |
| 38 | 686 | 91.1 | 747 | 6 | CQ818192 | CQ818192 Sequence |
| 39 | 686 | 91.1 | 747 | 6 | CS109203 | CS109203 Sequence |
| 40 | 686 | 91.1 | 747 | 6 | CS110208 | CS110208 Sequence |
| 41 | 686 | 91.1 | 747 | 6 | AR342863 | AR342863 Sequence |
| 42 | 587.5 | 78.0 | 793 | 6 | BD087298 | BD087298 Mammalian |
| 43 | 587.5 | 78.0 | 793 | 6 | CQ818185 | CQ818185 Sequence |
| 44 | 587.5 | 78.0 | 793 | 6 | CS109177 | CS109177 Sequence |
| 45 | 587.5 | 78.0 | 793 | 6 | CS110182 | CS110182 Sequence |

ALIGNMENTS

RESULT 1
LOCUS BD087297 926 bp DNA linear PAT 27-NOV-2002
DEFINITION Mammalian cytokine-like polypeptide-10.
ACCESSION BD087297.1 GI:22632907
VERSION JP 2001524313-A/1.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 926)
REFERENCE Conklin,D.C., Haldeman,B.A. and Grossmann,A.
Mammalian cytokine-like polypeptide-10
Patent: JP 2001524313-A 1 04-DEC-2001;
ZMOGENETICS INC
OS Homo sapiens (human)
PN JP 2001524313-A/1
PD 04-DEC-2001
PF 25-NOV-1998 JP 2000522245
PR 26-NOV-1997 US 08/979156
PI DARRIEL C CONKLIN,BETTY A HALDEMAN,ANGELICA GROSSMANN PC
C12N15/09,A01K67/027,A61K38/00,A61P1/02,A61P11/00, PC
A61P35/00,A61P37/02,A61P43/00,C07K14/52,C07K16/24,C07K16/42, PC
C12N15/00,

PC A6IK37/02
CC Mammalian cytokine-like polypeptide-10
FH Key Location/Qualifiers
FT CDS (45) . . (572) .
FEATURES
source Location/Qualifiers
1..926
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 3,22e-72 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-10-789-129-26 (1-144) x BD087297 (1-926)
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QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
201 GTGCAGACCAAGATGGAACATTTGACATCAGATCTTAAGAGAGAGCTGAGCTTTGCAA 260
QY 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
261 GACACAAAGCCGCGAATGATGCTGCTCCGCGCATTTGCTAAAGACTTAATCTTGAGAC 320
QY 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
321 AGGGATTATTAATACTACCAAGACCCCTGACATTAATCTCCGGAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
381 GCCAATTCCTTTCTTACATCAAGAAAGACCTCCGGCTGTGTCATGCCCATGACATGAC 440
QY 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
441 CATTTGGGGAGAGAGCAATGAAGAAATACAGCCAGATTCCTTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
501 GAACCTCAGGCAACAGCTGTGGAAGGCTTTGGGGGAACCTAGACATTTCTTCGCAATGAGTG 560
QY 141 GluGluThrGlu 144
561 GAGGAGACAGAA 572
DB
RESULT 2
CQ818183
LOCUS CQ818183 926 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 1 from Patent EP1424393.
ACCESSION CQ818183
VERSION CQ818183.1 GI:48426975
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Conklin,D.C., Haldeman,B.A. and Grossmann,A.
TITLE Mammalian cytokine-like polypeptide-10
JOURNAL Patent: EP 1424393-A 1 02-JUN-2004;
Zymogenetics Inc (US)
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source Location/Qualifiers
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45..575
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/db_xref="GI:4826976"
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ALGSDIILLQWMEETE"
ORIGIN
Alignment Scores:
Pred. No.: 3,22e-72 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-10-789-129-26 (1-144) x CQ818183 (1-926)
QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
141 TGTGTATGCGCCCAAACTTCAGAAATACGAAATGATTTCTGACATACGGGCACT 200
QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
201 GTGCAGACCAAGATGGAACATTTGACATCAGATCTTAAGAGAGAGCTGAGCTTTGCAA 260
QY 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
261 GACACAAAGCCGCGAATGATGCTGCTCCGCGCATTTGCTAAAGACTTAATCTTGAGAC 320
QY 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
321 AGGGATTATTAATACTACCAAGACCCCTGACATTAATCTCCGGAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
381 GCCAATTCCTTTCTTACATCAAGAAAGACCTCCGGCTGTGTCATGCCCATGACATGAC 440
QY 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
441 CATTTGGGGAGAGAGCAATGAAGAAATACAGCCAGATTCCTTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
501 GAACCTCAGGCAACAGCTGTGGAAGGCTTTGGGGGAACCTAGACATTTCTTCGCAATGAGTG 560
QY 141 GluGluThrGlu 144
561 GAGGAGACAGAA 572
DB
RESULT 3
CS109174
LOCUS CS109174 926 bp DNA linear PAT 22-JUN-2005
DEFINITION Sequence 1 from Patent WO2005052001.
ACCESSION CS109174
VERSION CS109174.1 GI:68148023
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Xu,W., Kindsvogel,W.R., Chen,Z., Hughes,S.D., Chandrasekhar,Y.A.,
Dillon,S.R., Lehner,J.M., Siadak,A.W., Sivakumar,P.V. and
Moore,M.D.
TITLE Anti-IL-20 receptor antibodies and binding partners and methods of
using in inflammation

JOURNAL Patent: WO 2005052001-A 1 09-JUN-2005;

ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers

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/note="unnamed protein product"

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/translation="MKASLAFSLSAAYLLTPSTGKTLNLGSCVATNLQELRN

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ALGELDILLQMEETE"

ORIGIN

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 3,22e-72 | Length: | 926 |
| Score: | 753.00 | Matches: | 144 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-10-789-129-26 (1-144) x CS109174 (1-926)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAnGlyPheSerAspIleArgIleSer 20

DB 141 TGTGTGATGCGCACAAACCTTCAGAAATACGAAATGATTTCTTGACATACGGGGCAGT 200

QY 21 ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40

DB 201 GTGCAAGCCAAAGATGAAACATTAACATGACAAATCTTAAGAGAGACTGAGCTTTGCAA 260

QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60

DB 261 GACACAAAGCCTGCGAATGATGCTGCTCCCTGCGCCATTTGCTAAGACTCTAATCTGAA 320

QY 61 ArgValIlePheIleAsnTyrGlnThrProAspHisTyrThrLeuArgIleSerSerLeu 80

DB 321 AGGTAATTTAAATACTACAGACCCCTGACATTAATCTCTCCGAAAGATGACGAGCTC 380

QY 81 AlaAsnSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100

DB 381 GCCAATTCCTTTTACCATCAAGAGAGACCTCCGCTCTGTCATGCCCCACATGACATGC 440

QY 101 HisCysGlyGluGluAlaMetIleIleIleIleIleIleIleIleIleIleIleIleIle 120

DB 441 CATTGTGGGAGAGAGCATGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

QY 121 GluProGlnAlaIleValIleValIleValIleValIleValIleValIleValIleVal 140

DB 501 GAACCTCAGGAGCAGTGTGAAAGCTTTGGGGGAACTAGACATCTTCTGCAATGATG 560

QY 141 GluGluThrGln 144

DB 561 GAGGAGACAGAA 572

QY 561 GAGGAGACAGAA 572

RESULT 4 CS110179 926 bp DNA linear PAT 22-JUN-2005

LOCUS CS110179

DEFINITION Sequence 1 from Patent WO2005052000.

ACCESSION CS110179

VERSION CS110179.1 GI:68148437

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

REFERENCE 1

AUTHORS

Xu, W., Kindsvogel, W.R., Chen, Z., Hughes, S.D., Chandrasekhar, Y.A.,

Dillon, S.R., Lehner, J.M., Siadak, A.W., Sivakumar, P.V. and

Moore, M.D.

Anti-I1-20 antibodies and binding partners and methods of using in

inflammation

JOURNAL Patent: WO 2005052000-A 1 09-JUN-2005;

ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

45..575

/note="unnamed protein product"

/codon_start=1

/protein_id="CAJ09906.1"

/db_xref="GI:68148438"

/translation="MKASLAFSLSAAYLLTPSTGKTLNLGSCVATNLQELRN

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HYTLRKISLSLSPFLTKKDLRLCHAHNTCHGSEAMKKSQIISHFEKLEPQAAYVK

ALGELDILLQMEETE"

ORIGIN

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 3,22e-72 | Length: | 926 |
| Score: | 753.00 | Matches: | 144 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-10-789-129-26 (1-144) x CS110179 (1-926)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAnGlyPheSerAspIleArgIleSer 20

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QY 21 ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40

DB 201 GTGCAAGCCAAAGATGAAACATTAACATGACAAATCTTAAGAGAGACTGAGCTTTGCAA 260

QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60

DB 261 GACACAAAGCCTGCGAATGATGCTGCTCCCTGCGCCATTTGCTAAGACTCTAATCTGAA 320

QY 61 ArgValIlePheIleAsnTyrGlnThrProAspHisTyrThrLeuArgIleSerSerLeu 80

DB 321 AGGTAATTTAAATACTACAGACCCCTGACATTAATCTCTCCGAAAGATCAGAGCTC 380

QY 81 AlaAsnSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100

DB 381 GCCAATTCCTTTTACCATCAAGAGAGACCTCCGCTCTGTCATGCCCCACATGACATGC 440

QY 101 HisCysGlyGluGluAlaMetIleIleIleIleIleIleIleIleIleIleIleIleIle 120

DB 441 CATTGTGGGAGAGAGCATGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500

QY 121 GluProGlnAlaIleValIleValIleValIleValIleValIleValIleValIleVal 140

DB 501 GAACCTCAGGAGCAGTGTGAAAGCTTTGGGGGAACTAGACATCTTCTGCAATGATG 560

QY 141 GluGluThrGln 144

DB 561 GAGGAGACAGAA 572

RESULT 5 AR342856 926 bp DNA linear PAT 17-AUG-2003

LOCUS AR342856

DEFINITION Sequence 1 from patent US 6576743.

ACCESSION AR342856

VERSION AR342856.1 GI:33738131

KEYWORDS

SOURCE

Unknown.

ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 926)
AUTHORS Conklin,D.C. and Haldeman,B.A.
TITLE Mammalian cytokine-like polypeptide-10
JOURNAL Patent: US 6576743-A 1 10-JUN-2003;
ZymoGenetics, Inc.; Seattle, WA
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"
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Alignment Scores:
Pred. No.: 3,226-72 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-789-129-26 (1-144) x AR342856 (1-926)
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QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 201 GTGCAGACCAAGATGAGAAACATTTGACATCAGATCTTAAGAGAGACTGAGCTTTGCAA 260
QY 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAACCTCGCAATGATGCTGCTCCGCGCATTTGTAGACCTTATCTGAGAC 320
QY 61 ArgValIlePheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB 321 AGGGTATTTAAATACTACAGACCCCTGACATTAATCTCCGGAAGATCAGACCTTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAATTCCTTCTTACATCAAGAAAGACCTCCGGCTCTGTATCATCCCAATGACATGC 440
QY 101 HisCysGlyGluGlnAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
DB 441 CATTTGGGGAGAGAACCAATGAAAGAAATACAGCCAAATCTTGTACATTTGAAAAGCTG 500
QY 121 GluProGlnAlaIleValIleValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
DB 501 GAACCTCAGGACGACGATGTTGAAAGGCTTTGGGGAACTAGACATTTCTTCTGCAATGATG 560
QY 141 GluGluThrGlu 144
DB 561 GAGGAGACAGAA 572
RESULT 6
AF224266 926 bp mRNA linear PRI 24-JAN-2001
LOCUS Homo sapiens four alpha helix cytokine (ZCYTO10) mRNA, ZCYTO10-1
DEFINITION
AF224266 Homo sapiens four alpha helix cytokine (ZCYTO10) mRNA, ZCYTO10-1
accession AF224266
version AF224266.1 GI:7109206
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 926)
REFERENCE
AUTHORS Blumberg,P., Conklin,D., Xu,W.F., Grossmann,A., Brendler,T.,
Carollo,S., Eagan,M., Foster,D., Haldeman,B.A., Hammond,A.,
Haugen,H., Jelinek,L., Kelly,J.D., Madden,K., Maurer,M.F.,
Parish-Novak,J., Prunkard,D., Saxon,S., Sprecher,C., Waggle,K.,

West,J., Whitmore,T.E., Yao,L., Kuechle,M.K., Dale,B.A. and
Chandrasekhar,Y.A.
Interleukin 20: discovery, receptor identification, and role in
epidermal function
Cell 104 (1), 9-19 (2001)
11163236
JOURNAL
PUBMED
2 (bases 1 to 926)
AUTHORS Conklin,D., Grossmann,A., Haldeman,B. and O'Hara,P.
TITLE Homo sapiens four alpha helix cytokine allele 1
JOURNAL Unpublished
REFERENCE
AUTHORS Conklin,D., Grossmann,A., Haldeman,B. and O'Hara,P.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2000) Biomolecular Informatics, ZymoGenetics,
Inc., 1201 Eastlake Ave. East, Seattle, Wa. 98102, USA
FEATURES
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ALGEBIDILQWMBETE"
ORIGIN
Alignment Scores:
Pred. No.: 3,226-72 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-789-129-26 (1-144) x AF224266 (1-926)
QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTATCGCCCAAAACCTTCAGGAAATACGAAATGCAATTTCTGACATACGGGCACT 200
QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 201 GTGCAGACCAAGATGAGAAACATTTGACATCAGATCTTAAGAGAGACTGAGCTTTGCAA 260
QY 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAACCTCGCAATGATGCTGCTCCGCGCATTTGTAGACCTTATCTGAGAC 320
QY 61 ArgValIlePheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB 321 AGGGTATTTAAATACTACAGACCCCTGACATTAATCTCCGGAAGATCAGACCTTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAATTCCTTCTTACATCAAGAAAGACCTCCGGCTCTGTATCATCCCAATGACATGC 440
QY 101 HisCysGlyGluGlnAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
DB 441 CATTTGGGGAGAGAACCAATGAAAGAAATACAGCCAAATCTTGTACATTTGAAAAGCTG 500
QY 121 GluProGlnAlaIleValIleValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140

Db 501 GAACCTCAGGACGAGCTTGAGGCTTGGGGGAACTAGACATTCCTCGAATGANG 560
 Oy 141 GUGUThrglu 144
 Db 561 GAGGAGACGAA 572

RESULT 7
 CS123418 462 bp DNA linear PAT 16-JUL-2005
 LOCUS Sequence 18 from Patent WO2005058946.
 DEFINITION CS123418
 ACCESSION CS123418
 VERSION CS123418.1 GI:70911957
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.

REFERENCE
 1
 AUTHORS Chan, C.
 TITLE Methods for enhancing expression of recombinant proteins
 JOURNAL Patent: WO 2005058946-A 18 30-JUN-2005;
 ZymoGenetics, Inc. (US)
 FEATURES
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ORIGIN

Alignment Scores:
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 Score: 749.00 Matches: 143
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 Query Match: 99.47% Indels: 0
 DB: 6 Gaps: 0

US-10-789-129-26 (1-144) x CS123418 (1-462)

Oy 1 CysVal111eAl1ThrAsnLeuGlnGlu11eArgAnGlyPheSerAsp11eArgGlySer 20
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 Oy 21 ValGlnAla1eAspG1yAsn11eAsp11eArg11eLeuArgThrgl1eSer1eLeuGln 40
 Db 88 GTGCAAGGCCAAGATGTAACTGACATTCCTGATCCGTGCGTACCAAGTCTCTGCAG 147
 Oy 41 AspThr1ySPro1eAsnArgCysCysLeuLeuArgH1sLeuLeuArgLeuTyr1eLeuAsp 60
 Db 148 GACACCAAAACCGGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 207
 Oy 61 ArgVal1Phe1yAsnTyrGln1ThrProAspH1sTyrThrLeuArg1y1eSer1eLeu 80
 Db 208 CGTGTTCCTCAAAAACATACACAGCCCGGACCACTATACCTCGTAAATCAGCAGCTCG 267
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 Db 268 GCAACCTCCTTCCTCAACATCAAAAAGACCTGCTGTGTGCAAGCCCACTGACCTGCGC 327
 Oy 101 H1sCysG1yG1uG1uAla1eMet1y1y1ySerGln11eLeuSerH1sPheG1u1y1eLeu 120
 Db 328 CACTGTGTGAGGAAGCAATGAAAAATACAGCCAGATTCTTACGCCACTTCAAAAACCTG 387
 Oy 121 GluProGlnAla1eVal1y1eAla1eLeuG1y1eLeuAsp11eLeuLeuG1n1r1yPheT 140
 Db 388 GAACCGCAGGCGAGCTGCTGTAAGCTCTGCGGTGAACCTGGAATCTCTGCTGCAAGTGATG 447
 Oy 141 GUGUThrglu 144
 Db 448 GAGGAGACCGAA 459

RESULT 8

BC069311
 LOCUS 531 bp mRNA linear PRI 06-JUL-2005
 DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96907
 IMAGE:7262116), complete cds.
 ACCESSION BC069311
 VERSION BC069311.1 GI:47480994
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.

REFERENCE
 1 (bases 1 to 531)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheeter, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Topfberg, S.,
 Carrinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullen, S.J., Bosak, S.A., McSwan, P.J.,
 McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bonfield, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalins, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 531)

CONSRMT
 TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
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JOURNAL
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 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 CONSRMT

REMARK
 COMMENT

NIH MGC Project
 Direct Submission
 Submitted (25-APR-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Baylor Human Genome Sequencing Center
 cDNA Library Preparation: Baylor Human Genome Sequencing Center
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgdbcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hult, S.W., Louised, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Navevati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNI at: <http://image.llnl.gov>
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ORIGIN
Alignment Scores:
Pred. No.:      4,73e-72      Length:      531
Score:          749.00      Matches:      143
Percent Similarity: 100.00%      Conservative: 1
Best Local Similarity: 99.31%      Mismatches: 0
Query Match:    99.47%      Indels:      0
DB:             8      Gaps:      0

US-10-789-129-26 (1-144) x BC069311 (1-531)

QY      1  CysValIleAlaThrArenLeuGlnIleArgAsnGlyPheSerAspIleArgGlySer 20
DB      97  TGTGTATCGCCCAACCTTCAGAAATACGAAATGATTTTCTGAGATACGGGCGAGT 156
QY      21  ValGlnAlaIleAspGlyAenIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB      157  GTTCAGACCCAAAGATGGAACATTTGACATCAGATCTTAAGAGGAGCTGATCTTTGGCA 216
QY      41  AspThrIleBProIalaAnaGysCysLeuLeuArgHisLeuLeuArgLeuIleuAsp 60
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IMAGE:7262128), complete cds.
ACCESSION      BC069364
VERSION      BC069364.1
KEYWORDS      MGC.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 531)
Strausberg,R.L., Peingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D.,

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TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT

FEATURES

source

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 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

gene

CDS

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL ac: <http://image.llnl.gov>
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 ALGEIDILQWMEETE"

ORIGIN

Alignment Scores:

Pred. No.: 4,73e-72 Length: 531
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
DB: 8 Gaps: 0

US-10-789-129-26 (1-144) x BC069364 (1-531)

QY 1 CysVal111eAlaThraAsnLeuGlnGlu111eAtgAsnGlyPheSerAsp111eArgGlySer 20
DB 97 TGTGTGATTCGCCCAAACTTCAGAAATATACCAAAATGATTTCTTCAGATACGGGGCAGT 156
QY 21 ValGlnAlaLysAspGlyAsn111eAsp111eArg111eLeuArgArgThrGlnSerLeuGln 40
DB 157 GTGCAAGCCAAAGATGAGAAACATTAACATGAGAAATCTTAAGAGAGACATGAGCTTTGCAA 216
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VERSION BC069398.1 GI:47481040
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 531)
AUTHORS Straubeberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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CONSRM TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
CONSRM
TITLE
JOURNAL
REMARK
COMMENT

Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 531)

NIH MGC Project
Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louisege, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Navavati,
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ORIGIN
Alignment Scores:
Pred. No.: 4,73e-72 Length: 531
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
DB: 8 Gaps: 0

US-10-789-129-26 (1-144) x BC069398 (1-531)

QY 1 CysVal111eAlaThraAsnLeuGlnGlu111eAtgAsnGlyPheSerAsp111eArgGlySer 20
DB 97 TGTGTGATTCGCCCAAACTTCAGAAATATACCAAAATGATTTCTTCAGATACGGGGCAGT 156
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| ACCESSION | | | IMAGE:262152), complete cds. |
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| KEYWORDS | | | BC069425.1 GI:47479503 |
| SOURCE | | | MGC. |
| ORGANISM | | | Homo sapiens (human) |
| REFERENCE | | | |
| AUTHORS | | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 531) Straubeberg RL, Feingold EA, Gronow LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shemmen CM, Schuler GD, Altschuld SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang Y, Heish F, Datchenko I, Marusina K, Farmer AD, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Schaefer TE, Brownstein MJ, Ustin TB, Yoshiyuki S, Canning P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullaly SJ, Bobak SA, McEwan PJ, McKernan KJ, Malek JA, Gunnaratne PH, Richardson S, Worley KC, Hale S, Garcia AM, Gay LJ, Huliyk SW, Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Keckeman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butlerfield IS, Krzywinski M, Skalska U, Smialov DE, Schermer A, Schein JE, Jones SJ and Marra MA. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 531) Director MGC Project. Direct Submission Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.ncl.nih.gov Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: Baylor Human Genome Sequencing Center cDNA Library Preparation: Baylor Human Genome Sequencing Center |
| REMARK | | | |
| COMMENT | | | |

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILIN)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hilyk, S.W., Louised, H.,
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 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRBR Plate: 1 Row: f Column: 2.

FEATURES
source

gene

CDS

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| Pred. No.: | 4.73e-72 |
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| Percent Similarity: | 100.00% |
| Best Local Similarity: | 99.31% |
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| Conservative: | 1 |
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US-10-789-129-26 (1-144) x BC069425 (1-531.

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| Qy | 101 | hiscyaglygluglualametylvlytyrserintlleuenserthaphcglulubreu | 120 |

| Db | 397 | CATTGGGGGAGGAACATGAAGAAATACAGCCAGATTCTGAGTCATCTTGAAAAGCTG | 456 |
|------------|--|--|-----------------------------|
| Qy | 121 | GIUFGGIALAAlaValVallyAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMet | 140 |
| Db | 457 | GAACCTCAGGCGACGAGCTGTGTGAAGCTTTGGGGGAACTAGACATCTTCTGCAATGATG | 516 |
| Qy | 141 | GIUGIUTTHGlu | 144 |
| Db | 517 | GAGGAGACAGAA | 528 |
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| DEFINITION | Homo sapiens Interleukin 20, mRNA (CDNA clone MGC:196955 | | |
| ACCESSION | BC069449 | | |
| VERSION | BC069449.1 GI:47480911 | | |
| KEYWORDS | MGC. | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. | | |
| AUTHORS | 1 (bases 1 to 531) | | |
| REFERENCE | Straussberg RL, Feingold EA, Grouse LH, Derge UC, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh P, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Ueda TB, Tomshiyaki S, Carninci P, Prange C, Raha SS, Loquellano ND, Nadin TB, Tohyiaki S, Carninci P, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Huiyk SW, Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Kettelman M, Madan A, Rodriguez S, Sanchez A, Whitting M, Madan A, Young AC, Shvchenko Y, Bouffard GS, Blakeley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood U, Schmutz J, Wyers RM, Butcherfield JS, Krzywinski M, Skalska U, Smalins DB, Scherch A, Schein JE, Jones SJ and Marra MA. | | |
| | Mammalian Gene Collection Program Team | | |
| CONSRMT | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences | | |
| TITLE | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) | | |
| JOURNAL | 1247932 | | |
| PUBMED | 2 (bases 1 to 531) | | |
| REFERENCE | Director MGC Project. | | |
| AUTHORS | Direct Submission | | |
| TITLE | Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA | | |
| JOURNAL | NIH-MGC Project URL: http://mgc.nci.nih.gov | | |
| REMARK | Contact: MGC help desk | | |
| COMMENT | Email: gcgabs-remail.nih.gov | | |
| REMARK | Tissue Procurement: Baylor Human Genome Sequencing Center | | |
| | cDNA Library Preparation: Baylor Human Genome Sequencing Center | | |
| REMARK | cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) | | |
| | DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center | | |
| REMARK | Center code: BCM-HGSC | | |
| | Web site: http://www.hgsc.bcm.tmc.edu/cdna/ | | |
| REMARK | Contact: amgdbcm.tmc.edu | | |
| | Gunnarsson, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Lousseng, H., Kovis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Navaretti, A.N., Gibbs, R.A. | | |
| REMARK | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov | | |
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ALIGNMENT SCORES:

Alignment Scores:
Pred. No.: 4.73e-72 Length: 531
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
DB: Gaps: 0

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LOCUS Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96967
DEFINITION IMAGE:7262176), complete cds.
ACCESSION BC069487
VERSION BC069487.1 GI:47480770

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
CONSRM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT

MGC.
Homo sapiens (human)
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
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Straussberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
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Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
1447932
2 (bases 1 to 531)
Director MGC Project.
Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: gcabs-remail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyik, S.W., Louised, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
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ORIGIN
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Pred. No.: 4,73e-72 Length: 531
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
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DB 517 GAGGAGACAGAA 528
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DEFINITION Homo sapiens interleukin 20, mRNA (cDNA clone MGC:96884
IMAGE:7262093), complete cds.
ACCESSION BC069523
VERSION BC069523.1 GI:47479431
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

Helton E, Kettelman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield JS, Krzywinski MI, Skalska U, Mammalian Gene Collection Program Team
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
 PUBMED
 12477932

REFERENCE
 2 (bases 1 to 531)
 Director MGC Project.
 Direct Submission
 Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Baylor Human Genome Sequencing Center
 CDNA Library Preparation: Baylor Human Genome Sequencing Center
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loubeeged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

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ORIGIN
 Alignment Scores:
 Pred. No.: 4.73e-72 Length: 531
 Score: 749.00 Matches: 143
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.31% Mismatches: 0
 Query Match: 99.47% Indels: 0
 DB: 8 Gaps: 0
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 LOCUS Homo sapiens interleukin 20, mRNA (CDNA clone MGC:96884
 IMAGE:7262105), complete cds.
 BC069559
 BC069559.1 GI:47480991
 MGC.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
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 Helton E, Kettelman M, Madan A, Rodriguez S, Sanchez A, Whiting M,
 Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
 Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
 Schmutz J, Myers RM, Butterfield JS, Krzywinski MI, Skalska U,
 Smilansky DE, Scherch A, Schein JE, Jones SJ and Marra MA.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

CONSRM
 TITLE
 Mammalian Gene Collection Program Team
 JOURNAL
 PUBMED
 12477932

REFERENCE
 2 (bases 1 to 531)
 Director MGC Project.
 Direct Submission
 Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Guanararte, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Loulesged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Manavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
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ORIGIN

Alignment Scores:

Pred. No.: 4,73e-72 Length: 531
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
DB: 8 Gaps: 0

US-10-789-129-26 (1-144) x BC069559 (1-531)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
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Search completed: December 28, 2005, 15:08:47
Job time : 2947 secs

PR 12-AUG-2002; 2002JP-00234880.
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XX
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XX WPI; 2004-320878/30.
XX P-PSDB; ADM95041.
XX
XX Agent useful for prevention and/or treatment of colon cancer, comprises
PT Interleukin 20 (IL-20), IL-20 receptor alpha chain, IL-20 receptor beta
PT chain.
XX
XX
XX Disclosure; SEQ ID NO 10; 50pp; Japanese.
XX
XX This invention relates to a novel agent for prevention and/or treatment
CC of colon cancer, comprising of the interleukin 20 (IL-20) receptor alpha
CC chain, its partial peptide or salt. The invention may be useful for the
CC development of compounds with a cytostatic activity. The invention is
CC useful for preventing and/or treating colon cancer. A diagnostic agent is
CC useful for diagnosis of colon cancer. By using IL-20, IL-20 receptor, its
CC salt or its peptide, compounds that have altered binding property towards
CC them can be efficiently screened. The present sequence is that of a gene
CC which encodes the human interleukin-20 protein and which is related to
CC the invention.
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Pred. No.: 5.13e-87 Length: 528
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-789-129-26 (1-144) x ADM95042 (1-528)
QY 1 CysValIleAlaThrAsnLeuGlnIuileArgAsnGlyPheSerAspIleArgGlySer 20
DB 97 TGTGTATCGCCCAAACTTCAGAAATACGAAATGATTTCTGACATACGGGCGACT 156
QY 21 ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 157 GTCCAAAGCCAAAGATGGAACATTCGACATCGAATCTTAAGAGAGACTGATCTTTGCCA 216
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuIleuAsp 60
DB 217 GACACAAAGCCTCGAATCGATGCTGCTCGCCATTTGCTAAGACTCTATCTGGAC 276
QY 61 ArgValPheIleAsnArgIleuThrProAspHisTyrThrLeuArgIleuSerSerLeu 80
DB 277 AGGGTATTTAAACCTACAGACCCCTGACCATTTATCTCCGGAAGATCAGCAGCTC 336
QY 81 AlaAsnSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
DB 337 GCCAATTCCTTTCTTACATCAAGAGAGACTCCGGCTCTGTCAATGCCACATGACATGC 396
QY 101 HisCysGlyGlnGlnAlaMetIleIleIleIleIleIleIleIleIleIleIleIleIle 120
DB 397 CATTTGGGGAGAGAGCAATGAAGAATATACGACCATTTCTGAGTCACTTGAAGAGCTG 456
QY 121 GlnProGlnAlaIleValIleIleIleIleIleIleIleIleIleIleIleIleIleIle 140
DB 457 GAACCTCAGGACAGAGTGTGAAGGCTTTGGGGGAACATGACATTTCTTGCAGATGATG 516
QY 141 GlnGlnThrGln 144
DB 517 GAGGAGACAGAA 528
RESULT 2
ADV42800 standard; cDNA; 531 BP.
ID XX
AC ADV42800;

XX
DT 10-MAR-2005 (first entry)
XX
XX Human psychoneuroendocrineimmune expressed sequence tag SEQ ID NO 428.
DE
XX
XX microarray; psychoneuroendocrineimmune; chronic fatigue;
XX non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2004108899-A2.
XX
XX 16-DEC-2004.
XX
XX 04-JUN-2004; 2004WO-US017686.
XX
XX 04-JUN-2003; 2003US-0475915P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Nicholson A, Vernon SD,
XX
XX WPI; 2005-031682/03.
XX
XX
XX New microarray comprising probes for genes involved in
PT psychoneuroendocrineimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
XX Claim 1; SEQ ID NO 428; 254pp; English.
XX
XX The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrineimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrineimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
XX Sequence 531 BP; 149 A; 129 C; 123 G; 130 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 5.18e-87 Length: 531
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-789-129-26 (1-144) x ADV42800 (1-531)
QY 1 CysValIleAlaThrAsnLeuGlnIuileArgAsnGlyPheSerAspIleArgGlySer 20
DB 97 TGTGTATCGCCCAAACTTCAGAAATACGAAATGATTTCTGACATACGGGCGACT 156
QY 21 ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 157 GTCCAAAGCCAAAGATGGAACATTCGACATCGAATCTTAAGAGAGACTGATCTTTGCCA 216
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuIleuAsp 60
DB 217 GACACAAAGCCTCGAATCGATGCTGCTCGCCATTTGCTAAGACTCTATCTGGAC 276
QY 61 ArgValPheIleAsnArgIleuThrProAspHisTyrThrLeuArgIleuSerSerLeu 80
DB 277 AGGGTATTTAAACCTACAGACCCCTGACCATTTATCTCCGGAAGATCAGCAGCTC 336
QY 81 AlaAsnSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
DB 337 GCCAATTCCTTTCTTACATCAAGAGAGACTCCGGCTCTGTCAATGCCACATGACATGC 396

QY 101 HISCYGGIYGIUGIUALAMETLYSYTYSERGINILEUUSERHISPHEGLIULYSLEU 120
 DB 397 CATTGGGGAGAGAACCATGAAGAAATACGCCAATTCTAGTCACTTGAAGAGCTG 456
 QY 121 GIUPROGINALALAVAlVallysalaleuGIYGIULEUASPIILEUENUGINTPMET 140
 DB 457 GAACCTCAGGACGACATTGTGAAGCTTTGGGGAACTAGACATCTTCTGCATGATGAG 516
 QY 141 GIUGIUTHRGIU 144
 DB 517 GAGGAGACAGAA 528

RESULT 3
 AAX77692
 ID AAX77692 standard; cDNA; 926 BP.
 XX
 AC AAX77692;
 XX
 DT 09-AUG-1999 (first entry)
 XX
 DE Human Zcyto10 allele 1 cDNA.
 XX
 KM Zcyto10; four alpha helix cytokine; vulnerary; cytosstatic; haemostatic;
 KM anti-inflammatory; anti-asthmatic; growth factor; maintenance factor;
 KM trachea; salivary gland; stomach; pancreas; muscle; gene therapy; cancer;
 KM proliferation; differentiation; modulator; gastrointestinal tract;
 KM oral cavity; asthma; tracheobronchial tract; bronchitis; wound healing;
 KM platelet count; thrombocytopenia; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 45..575
 FT /*tag= a
 FT /product= "Zcyto10"

WO9927103-A1.
 03-JUN-1999.
 25-NOV-1998; 98WO-US0252228.
 26-NOV-1997; 97US-00979156.
 (ZYMO) ZYMOGENETICS INC.
 Conklin DC, Haldeman BA, Grossmann A;
 WPI, 1999-357840/30.
 P-PSDB; AAY08661.
 New mammalian cytokine-like polynucleotide useful in the treatment of
 asthma and bronchitis.
 Claim 3; Page 63-64; 82pp; English.

This invention describes a novel mammalian four alpha helix cytokine
 designated Zcyto10 which has vulnerary, cytosstatic, anti-inflammatory,
 anti-asthmatic and haemostatic activity. Zcyto10 may be a growth and/or
 maintenance factor in the trachea and salivary glands, stomach, pancreas
 and muscle. Zcyto10 polynucleotides are useful as sources of primers and
 probes, and to determine if the Zcyto10 gene is present on chromosome 1,
 or to detect any mutations that may have occurred. Zcyto10
 polynucleotides are also useful as gene therapy reagents. The Zcyto10
 polynucleotide, its fragments, and antibodies, as well as compounds
 identified as having binding affinity to Zcyto10, should be useful in the
 treatment of conditions associated with abnormal physiology or
 development, including abnormal proliferation, e.g. cancerous conditions,
 or degenerative conditions or altered immunity. The products are also
 useful for modulating cell proliferation, cell differentiation or
 cytokine production in the prevention or treatment of conditions
 characterized by abnormal cell proliferation, cell differentiation or
 cytokine production. Zcyto10 polypeptides, agonists and antagonists may

CC be therapeutically useful in the regeneration of the gastrointestinal
 CC tract or oral cavity, as well as in the treatment of asthma, and other
 CC diseases of the tracheobronchial tract such as bronchitis. Zcyto10
 CC polypeptides may also be useful to promote wound healing, and to increase
 CC platelet count, e.g. in cancer patients who experience thrombocytopenia
 CC due to chemotherapy or radiation therapy
 XX

Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.17e-86 Length: 926
 Score: 753.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 2 Gaps: 0

US-10-789-129-26 (1-144) x AAX77692 (1-926)

QY 1 CysValIleAlaThrAspLeuGlnGluIleArgAsnGlyPheSerAspIleArgIlySer 20
 DB 141 TGTGTGATGCGCCAAACCTTCAGGAATACGAATGGATTTTCTGACATACGGGGCACT 200
 QY 21 ValGlnAlaYAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
 DB 201 GTGCAAGCCAAAGATGAAAGCACTTCACTCAGAACTTAAAGAGAGACTGACTTTGCA 260
 QY 41 AspThrIysPProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyIleuAsp 60
 DB 261 GACACAAAGCCGCGAATGATGATGCTGCTCCGCGCCCACTTGTAAAGACTATCTGGAC 320
 QY 61 ArgValPheIysAsnTyGIlnThrProAspHisTyThrIleuArgIlyIleSerSerLeu 80
 DB 321 AGGGATTATTAATACTACCAAGCCCTGACCAATTAATCTCCGGAAGATCAGCAGCCCTC 380
 QY 81 AlaAsnSerPheLeuThrIleIlyIysAspLeuArgLeuCysHisAlaHisMetThrCys 100
 DB 381 GCCAATTCCTTTCTTACCATCAAGAGAGACCTCCGCGCTCTGTGCATGCCACATGACATGC 440
 QY 101 HISCYGGIYGIUGIUALAMETLYSYTYSERGINILEUUSERHISPHEGLIULYSLEU 120
 DB 441 CATTGTGGGAGAGAAAGCAATGAGAAATACAGCCAGATTCTGAGTCACTTGAAGAGCTG 500
 QY 121 GIUPROGINALALAVAlVallysalaleuGIYGIULEUASPIILEUENUGINTPMET 140
 DB 501 GAACCTCAGGACGAGTTGTGAAGCTTTGGGGAACTAGACATCTTCTGCATGATGAG 560
 QY 141 GIUGIUTHRGIU 144
 DB 561 GAGGAGACAGAA 572

RESULT 4
 ACF05161
 ID ACF05161 standard; cDNA; 926 BP.
 XX
 AC ACF05161;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Polynucleotide encoding human interleukin-20.
 XX
 KM Human; interleukin-20; IL-20; cervical cancer; cytostatic; virucide;
 KM gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 45..575
 FT /*tag= a
 FT /product= "Human IL-20"
 FT sig_peptide 45..116
 FT /*tag= b
 FT mat_peptide 117..572

```

FT XX /+tag= c
PN XX WO2003051384-A1.
PD XX 26-JUN-2003.
XX XX
PF 17-DEC-2002; 2002WO-US040309.
XX XX
PR 17-DEC-2001; 2001US-0341783P.
XX XX
PA (LUNN/) LUNN P G.
XX XX
PI Chandrasekher YA, McKernan PA;
XX XX
DR WPI; 2003-569114/53.
DR P-PSDB; ABR62464.
XX XX
PT Inhibiting the growth and/or proliferation of cervical cancer cells,
PT useful for treating cervical cancer or human papilloma virus infection,
PT comprises bringing Interleukin-20 (IL-20) into contact with the cervical
PT cancer cells.
XX XX
PS Disclosure; Page 11-12; 26pp; English.
XX XX
CC The present sequence is that of a polynucleotide encoding human
CC Interleukin-20 (IL-20), including the signal sequence. The invention
CC relates to the use of IL-20 for treating cervical cancer or cells
CC infected with human papilloma virus. IL-20 can be administered alone or
CC in conjunction with radiation or chemotherapeutic agents or surgical
CC excision of the involved cells or lesions
XX XX
SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.17e-86 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-789-129-26 (1-144) x ACF05161 (1-926)

QY 1 CysValIleAlaIhrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTGATCCGCCAACCCTTCAGAAATACGAATGGATTCTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaIAspArgIAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 201 GTGCAGCCCAAGATGGAAACATTGACATCAGAACTTTAAGAGAGACTGAGTCTTTGCCAA 260
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuIleuAsp 60
DB 261 GACACAAAGCCTCGAATCGATGCTGCTCTCGGCATTGTGTAAGACTCTATCTGGAC 320
QY 61 ArgValIlePheIAsnArgIleThrProAspHisIleThrLeuArgIleSerSerLeu 80
DB 321 AGGGTATTAAAACTAACACAGACCCCTGACATTATACCTCCGGAAGATCAGCAGCTC 380
QY 81 AlaAsnSerPheLeuThrIleIleIleCysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAATTCCTTTCTTACCATCAGAGAGACCTCCGGCTCTGTCTATGCCCATGACATGC 440
QY 101 HisCysGlyGlnGlnAlaMetIleCysIleSerGlnIleLeuSerHisPheGlnIleu 120
DB 441 CATTTGGGGAGAGAGCAATGAGAAATACAGCAGATTCTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGlnAlaIleValIleValIleGlnGlyGlnIleuAspIleLeuLeuGlnITTPMet 140
DB 501 GAACCTCAGCAGCAGAGTTGTGAAGGCTTTGGGGGAATCAGACATTTCTTTCGCAATGATG 560
QY 141 GluGlnThrGlu 144
DB 141 |||||

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DB 561 GAGGAGACAGAA 572
RESULT 5
AAD61821
ID AAD61821 standard; cDNA; 926 BP.
XX XX
AC AAD61821;
XX XX
DT 15-JAN-2004 (first entry)
XX XX
DE Human cytokine-like polypeptide-10 (Zcyto10) cDNA.
XX XX
KW Human; cytokine-like polypeptide-10; Zcyto10; therapy; thrombocytopoenia;
KW autoimmune disease; insulin-dependent diabetes mellitus; immune response;
KW rheumatoid arthritis; multiple sclerosis; infection; radiation therapy;
KW asthma; bronchitis; wound healing; periodontal disease; antiinflammatory;
KW psoriasis; eczema; dry skin; oral cavity; muscle atrophy; haemostatic;
KW cancer; vulnery; chromosome 1; gene; ss.
XX XX
OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT CDS 45..575
FT /+tag= a
FT /product= "Human Zcyto10"
FT sig_peptide 45..116
FT /+tag= b
FT mat_peptide 117..572
FT /+tag= c
FT /product= "Mature human Zcyto10"
XX XX
PN US6576743-B1.
XX XX
PD 10-JUN-2003.
XX XX
PF 17-MAY-1999; 99US-00313458.
XX XX
PR 26-NOV-1997; 97US-0066597P.
XX XX
PR 25-NOV-1998; 98US-00199586.
XX XX
PA (ZYMO) ZYMOGENETICS INC.
XX XX
PI Conklin DC, Haldeman BA;
XX XX
DR WPI; 2003-799828/75.
DR P-PSDB; AEM00889.
XX XX
PT Novel human cytokine-like polypeptide-10, Zcyto10, useful for treating
PT insulin-dependent diabetes mellitus, rheumatoid arthritis, multiple
PT sclerosis, asthma, psoriasis and inhibiting cancer cell growth.
XX XX
PS Disclosure; Col 29-30; 0pp; English.
XX XX
CC The invention relates to an isolated human cytokine-like polypeptide-10
CC (Zcyto10) polypeptide. Zcyto10 is useful for prevention or treatment of
CC conditions characterised by improper cell proliferation, cell
CC differentiation or cytokine production. Zcyto10 is useful for treating
CC autoimmune diseases such as insulin-dependent diabetes mellitus,
CC rheumatoid arthritis, multiple sclerosis, etc., by inhibiting cellular
CC immune response. The invention is useful for inhibiting cancer cell
CC growth or proliferation, for stimulating immune system to combat
CC microbial or viral infections, for increasing platelet production, and
CC thus useful in cancer patients who experience thrombocytopaenia due to
CC cancer therapy or radiation therapy. Zcyto10 is useful in trachea-
CC specific or tracheobronchial-specific applications, such as in the
CC maintenance or would repair of the tracheobronchial epithelium or cells
CC underlying the same, in regulating mucous production or mucociliary
CC clearance of debris or in treatment of asthma, bronchitis or other
CC diseases of the tracheobronchial tract. Zcyto10 may also enhance wound
CC healing and promote regeneration of affected tissues which may be
CC especially useful in the treatment of periodontal disease. Zcyto10 can be
CC used to treat skin conditions such as psoriasis, eczema and dry skin in
CC general. Zcyto10 is useful for regenerating gastrointestinal tract or

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CC oral cavity and for modulating muscle tone in the tracheobronchial tract,
 CC and for treating muscle atrophy in the elderly, sick or bed-ridden.
 CC Zcyto10 is also useful for promoting wound healing. The present sequence
 CC is human Zcyto10 cDNA. The Zcyto10 gene is located on chromosome 10
 XX

Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 1.17e-86 | Length: | 926 |
|------------------------|----------|---------------|-----|
| Score: | 753.00 | Matches: | 144 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

US-10-789-129-26 (1-144) x ADG61821 (1-926)

```

QY 1 CysValIleAlaThrAsnLeuGlnIleArgAsnGlyPheSerAspIleArgIleSer 20
DB 141 TGTGTATCGCCCAAACTTCAGAAATACGAAATGATTTCTGACATACGGGCGAGT 200
QY 21 ValGlnAlaIleAspIleAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 201 GTGCAAGCCAAAGATGAAACATTCATCAGATCTTAAGAGAGAGCTGAGCTTTGCAA 260
QY 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCCCTGCGAATGATGATCTGCTCTGCGCATTTGCTAAGACTCTATCTGAC 320
QY 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB 321 AGGGATTTAAAACATACAGAACCCCTGACCATTAATCTCTCGGAAGATCAGCACTTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAATTCCTTTCTTACATCAAGAAAGAGACCTCCGCTGTGATCCCAATGACATGC 440
QY 101 HisCysGlyGluGlnIleMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
DB 441 CATTTGGGGAGAGAACATGAAAGAAATACAGCCAGATCTGATGATCTTTGAAAAGCTG 500
QY 121 GluProGlnAlaIleValIleValLysAlaLeuGluGluLeuAspIleLeuLeuGlnTyrMet 140
DB 501 GAACCTCAGCAGCAGAGTTGTGAAGGCTTTGGGGGAACCTAGACATTTCTTGCAGATGAG 560
QY 141 GluGluThrGlu 144
DB 561 GAGGAGACAGAA 572

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RESULT 6
 ADG46668
 ID ADG46668 standard; DNA; 926 BP.
 AC ADG46668;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human Zcyto10 DNA #1.
 XX
 XX cytokine-like polypeptide-10; Zcyto10; wound healing;
 KW platelet proliferation; wound repair; mucous production; asthma;
 KW bronchitis; tracheobronchial tract disease; periodontal disease;
 KW skin condition; psoriasis; eczema; dry skin; protein therapy; human;
 KW vulnery; respiratory; antibronchitic; dental; dermatological; gene; ds.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 45..575
 FT /tag= B
 FT /product= "Human Zcyto10 protein"
 FT sig_peptide 45..116
 FT /tag= a

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FT mat_peptide 117..572
FT /tag= C
FT /product= "Human mature Zcyto10 protein"
XX
XX US2003176657-A1.
XX
XX 18-SEP-2003.
XX
XX 15-APR-2003; 2003US-00413661.
XX
XX 26-NOV-1997; 97US-0066597P.
XX 25-NOV-1998; 98US-00199586.
XX 17-MAY-1999; 99US-00313458.
XX
XX (CONK/) CONKLIN D C.
XX (HALD/) HALDEMAN B A.
XX
XX Conklin DC, Haldeman BA;
XX
XX WPI; 2003-863865/80.
XX P-PsDB; ADG46669, ADG46679.
XX
XX Novel isolated mammalian cytokine-like polypeptide-10 (Zcyto10), useful
XX for treating asthma, bronchitis and other tracheobronchial damage.
XX
XX Disclosure; SEQ ID NO 1; 31pp; English.
XX
XX The present invention relates to novel mammalian cytokine-like
XX polypeptide-10 (Zcyto10) proteins and polynucleotides encoding such
XX proteins. Sequences of the invention are useful for promoting the healing
XX of wounds and for stimulating the proliferation of platelets. In
XX particular Zcyto10 polypeptides may be used in trachea-specific or
XX tracheobronchial-specific applications such as maintenance or wound
XX repair of the tracheobronchial epithelium or cells underlying it; in
XX regulating mucous production; mucociliary clearance of debris; in
XX treatment of asthma, bronchitis and other diseases of the
XX tracheobronchial tract. They are also used to promote regeneration of
XX affected tissues which may be especially useful in the treatment of
XX periodontal disease. Zcyto10 polypeptides can be used to treat skin
XX conditions such as psoriasis, eczema and dry skin in general. They are
XX also used in protein therapy. The present sequence is human Zcyto10 DNA.
XX
XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;

```

Alignment Scores:

| Pred. No.: | 1.17e-86 | Length: | 926 |
|------------------------|----------|---------------|-----|
| Score: | 753.00 | Matches: | 144 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

US-10-789-129-26 (1-144) x ADG46668 (1-926)

```

QY 1 CysValIleAlaThrAsnLeuGlnIleArgAsnGlyPheSerAspIleArgIleSer 20
DB 141 TGTGTATCGCCCAAACTTCAGAAATACGAAATGATTTCTGACATACGGGCGAGT 200
QY 21 ValGlnAlaIleAspIleAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 201 GTGCAAGCCAAAGATGAAACATTCATCAGATCTTAAGAGAGAGCTGAGCTTTGCAA 260
QY 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCCCTGCGAATGATGATCTGCTCTGCGCATTTGCTAAGACTCTATCTGAC 320
QY 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB 321 AGGGATTTAAAACATACAGAACCCCTGACCATTAATCTCTCGGAAGATCAGCACTTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAATTCCTTTCTTACATCAAGAAAGAGACCTCCGCTGTGATCCCAATGACATGC 440

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QY 101 H1aCyeg1yGluGlu1a1aMet1yS1yTySerGln1leuSerHispehGlu1yS1e1u 120
|||||
Db 441 CATTTGGGGAGGAGCAATGAAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGln1a1a1aVal1yVal1yS1a1e1uG1yGlu1e1uAsp1le1e1u1e1uG1n1TPMet 140
|||||
Db 501 GAACCTCAGGCGACAGTGTGAAAGCTTTGGGGAACTGACATCTCTCTGCAATGAGATG 560
QY 141 GluGluThrGlu 144
|||||
Db 561 GAGGAGACAGAA 572
RESULT 7
ADQ88066 standard; DNA; 926 BP.
ID ADQ88066 standard; DNA; 926 BP.
AC ADQ88066;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human Zcyto10 longer form DNA.
XX
KM Mammalian cytokine-like polypeptide-10; Zcyto10; cell proliferation;
cell differentiation; cytokine production; autoimmune disease;
insulin dependent diabetes mellitus; multiple sclerosis;
rheumatoid arthritis; cancer; wound healing; tissue regeneration;
platelet count; asthma; skin disease; psoriasis; eczema; dry skin;
antibiotic; neuroprotective; antirheumatic; antiarthritic; cytostatic;
immunostimulant; vulnery; antiasthmatic; antipsoriatic; dermatological;
gene therapy; human; gene; de.
XX
OS Homo sapiens.
XX
FH Key CDS Location/Qualifiers
FT CDS 45..575
FT /*tag= b
FT /product= "Human Zcyto10 protein"
FT sig_peptide 45..116
FT /*tag= a
FT mat_peptide 117..572
FT /*tag= c
FT /product= "Human mature Zcyto10 protein"
FT CDS 141..575
FT /*tag= d
FT /product= "Human Zcyto10 protein fragment"
FT /partial
FT /note= "No start codon"
XX
PN US2004142428-A1.
XX
PD 22-JUL-2004.
XX
PF 27-FEB-2004; 2004US-00789129.
XX
PR 26-NOV-1997; 97US-0066597P.
PR 25-NOV-1998; 98US-0019986P.
PR 15-APR-2003; 2003US-00413661.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Conklin DC, Haldeman BA;
XX
DR MPI; 2004-552564/53.
DR P-PSDB; ADQ88067, ADQ88077, ADQ88091.
XX
PT New Zcyto10 polypeptides and polynucleotides, useful for treating
autoimmune diseases (e.g. insulin dependent diabetes mellitus, multiple
sclerosis or rheumatoid arthritis), or skin conditions (e.g. psoriasis or
eczema).
XX
PS Disclosure; SEQ ID NO 1; 31pp; English.
XX

CC The present invention provides mammalian cytokine-like polypeptide-10
CC (Zcyto10) proteins and their encoding polynucleotides. The invention is
CC useful for treating conditions characterised by improper cell
CC proliferation, cell differentiation or cytokine production, specifically
CC for treating autoimmune diseases such as insulin dependent diabetes
CC mellitus, multiple sclerosis and rheumatoid arthritis and for inhibiting
CC cancer cell growth. The invention is also used to stimulate the immune
CC system, to enhance wound healing and promote regeneration of affected
CC tissues, to increase platelet count and to treat asthma and skin
CC conditions such as psoriasis, eczema and dry skin. The invention acts as
CC an antidiabetic, neuroprotective, antirheumatic, antiarthritic,
CC cytostatic, immunostimulant, vulnery, antiasthmatic, antipsoriatic and
CC dermatological agent. The invention is also used in gene therapy. The
CC present sequence is human Zcyto10 longer form DNA.
XX
SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,17e-86 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-789-129-26 (1-144) x ADQ88066 (1-926)
QY 1 CyVal11a1a1aThr1a1e1u1e1uG1n1u1e1a1g1a1n1y1p1e1s1e1a1p1e1a1g1y1s1e1r 20
141 TGTGTATGCGCCACAAACCTTCAGGAAATACGAAATGATTTCTTGACATACGGGGCAGT 200
QY 21 ValGln1a1y1a1a1y1a1n1l1e1a1p1e1a1g1l1e1e1u1a1r1y1a1r1y1e1u1e1u1n1 40
201 GTGCAAGCCAAAGATGAAACATTCACATCAATCTTAAAGAGACTAGCTTTGGCAA 260
QY 41 AspThr1y1p1e1a1a1a1y1a1n1l1e1a1p1e1a1g1l1e1e1u1a1r1y1a1r1y1e1u1e1u1n1 60
261 GACACAAAGCTCGCAATGATGCTGCTCCGCGCAATTTGCTAAGACTTATCTGAGC 320
QY 61 ArgVal1p1e1y1a1n1l1e1a1p1e1a1g1l1e1e1u1a1r1y1a1r1y1e1u1e1u1n1 80
321 AGGGTATTTAAACATCACAGACCCCTGACCATTAATCTCCGAAATCAGACCCCTC 380
QY 81 AlaSer1p1e1e1u1n1r1l1e1y1a1p1e1a1g1l1e1e1u1a1r1y1a1r1y1e1u1e1u1n1 100
381 GCCAATTCCTTCTTACATCAAGAGACCTCCGGCTGTATGCTCCACATGACATGC 440
QY 101 H1aCyeg1yGluGlu1a1aMet1yS1yTySerGln1leuSerHispehGlu1yS1e1u 120
|||||
Db 441 CATTTGGGGAGGAGCAATGAAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGln1a1a1aVal1yVal1yS1a1e1uG1yGlu1e1uAsp1le1e1u1e1uG1n1TPMet 140
|||||
Db 501 GAACCTCAGGCGACAGTGTGAAAGCTTTGGGGAACTGACATCTCTCTGCAATGAGATG 560
QY 141 GluGluThrGlu 144
|||||
Db 561 GAGGAGACAGAA 572
RESULT 8
ADRI6327
ID ADRI6327 standard; DNA; 926 BP.
XX
AC ADRI6327;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human cytokine-like polypeptide-10 (Zcyto10) long form DNA.
XX
KM Cytokine-like polypeptide-10; Zcyto10; therapy; asthma; infection;
psoriasis; eczema; dry skin; wound healing; platelet proliferation;
human; gene; de.
XX

```
OS Homo sapiens.
XX Location/Qualifiers
XX Key 45..575
XX CDS
FT
FT sig_peptide
FT /product= "Zcyto10 long form protein"
FT /tag= b
FT 45..116
FT mat_peptide
FT 117..572
FT /tag= a
FT /product= c
FT /product= "Mature Zcyto10 long form protein"
XX
XX US2004152878-A1.
XX
XX 05-AUG-2004.
XX
XX
XX 27-FEB-2004; 2004US-00789968.
XX
XX 26-NOV-1997; 97US-0066597P.
XX 25-NOV-1998; 98US-00199586.
XX 15-APR-2003; 2003US-00413661.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Conklin DC, Haldeman BA;
XX
XX WPI; 2004-580197/56.
XX
XX P-PsDB; ADR16328, ADR16338.
XX
XX
XX New isolated antibody that binds to a Zcyto10 polypeptide, useful for
XX treating asthma, microbial or viral infections, and for promoting the
XX healing of wounds, psoriasis, eczema or dry skin.
XX
XX Disclosure; SEQ ID NO 1; 32pp; English.
XX
XX
XX The invention relates to novel cytokine-like polypeptide-10 (Zcyto10)
XX polypeptides and polynucleotides. Zcyto10 sequences are useful for
XX treating asthma, microbial or viral infections, psoriasis, eczema or dry
XX skin, for promoting the healing of wounds and for stimulating the
XX proliferation of platelets. The present sequence is human Zcyto10 DNA.
XX
XX
XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1,17e-86 Length: 926
XX Score: 753.00 Matches: 144
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 13 Gaps: 0
XX
XX US-10-789-129-26 (1-144) x ADR16327 (1-926)
XX
XX
XX 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
XX 141 TGTGTATGCGCCAAACCTTCAGAAATACGAAATGATTTCTGACATACGGGGCACT 200
XX
XX 21 ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
XX 201 GTGCAAGCCAAAGATGAAACATTCAGATCATCAGAACTTAAAGAGAGCTGAGTCTTGCAA 260
XX
XX 41 AspThrIleProIleAlaAsnArgCysGlyLeuLeuArgHisLeuLeuArgLeuIleuAsp 60
XX 261 GACCAAAAGCCCTCGAATGCATCTCTCTCCGCAATTCCTAAAGACTCTATCTGGAC 320
XX
XX 61 ArgValIlePheIleAsnTyrglnThrProAspHisIleThrLeuArgGlyIleSerSerLeu 80
XX 321 AGGATATTTAAAAAATACCAAGACCCCTGACCATTAATCTCCGGAAGATACAGACCTTC 380
XX
XX 81 AlaSerSerPheLeuThrIleIleValIleAspLeuArgLeuCysHisAlaHisIleThrCys 100
XX 381 GCCAATTCCTTCTTCACTCAACAAAGAGACCTCCGCTCTGTCATGCCCAATGACATGC 440
XX DB
```

```
Qy 101 HisCysGlyGluGluAlaMetIleValIleTyrSerGlnIleLeuSerHisPheGluIleLeu 120
Db 441 CATTTGTGGGAGAGAGCAATGAAATACAGCCAGATTCTGACTCACTTTGAAAAGCTG 500
Qy 121 GluProGlnAlaValIleValIleValIleGlyIleLeuAspIleLeuGlnTyrMet 140
Db 501 GAACCTCAGGACAGAGTTGTGAAGGCTTTGGGGGAACTAGACATTTCTTGCATGATG 560
Qy 141 GluGluThrGlu 144
Db 561 GAGGAGACAGAA 572
XX
XX RESULT 9
XX ID ADR24325 standard; DNA; 926 BP.
XX AC
XX ADR24325;
XX
XX 21-OCT-2004 (first entry)
XX
XX DE Breast cancer prognosis marker #186.
XX
XX KW de; breast cancer; prognosis; gene expression; diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN NO2004065545-A2.
XX
XX PD 05-AUG-2004.
XX
XX PF 15-JAN-2004; 2004WO-US001100.
XX
XX PR 15-JAN-2003; 2003US-00342887.
XX
XX PA (ROSE-) ROSETTA IMPHARMATICS LLC.
XX PA (NECA-) NETHERLANDS CANCER INST.
XX
XX PI Van't Veer LJ, He Y;
XX
XX WPI; 2004-593473/57.
XX
XX
XX Classifying a breast cancer patient according to prognosis comprises
XX PT determining the similarity between the level of expression of each of
XX PT five genes in a cell sample taken from patient, to control levels.
XX
XX
XX Disclosure; SEQ ID NO 186; 226pp; English.
XX
XX
XX The invention relates to a method of classifying a breast cancer patient
XX according to prognosis by determining the similarity between the level of
XX expression of each of five genes for which markers are listed in the
XX CC specification, in a cell sample taken from the breast cancer patient, to
XX CC control levels of expression for each respective five genes to obtain a
XX CC patient similarity value. The methods are useful for classifying a breast
XX CC cancer patient according to prognosis. Kits and computer program products
XX CC are useful for data analysis using the diagnostic, prognostic and
XX CC statistical methods of the invention. This sequence corresponds to a
XX CC marker used in the method of the invention.
XX
XX
XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1,17e-86 Length: 926
XX Score: 753.00 Matches: 144
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 13 Gaps: 0
XX
XX US-10-789-129-26 (1-144) x ADR24325 (1-926)
XX
XX
XX 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
XX 141 TGTGTATGCGCCAAACCTTCAGAAATACGAAATGATTTCTGACATACGGGGCACT 200
XX DB
```

```
QY 21 ValGlnAlaIyAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerIleuGln 40
DB 201 GTGCAGGCCAAGATGAGAAACATTGACATCAGAAATCTTAAGAGAGACTGAGTCTTTCGAA 260
QY 41 AspThrIysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrIleuAsp 60
DB 261 GACACAAAGCCTGGCAATGATGCTGCTCCCTGCGCCATTGCTAAGACTCTATCTTGAC 320
QY 61 ArgValPheIysAsnTyrGlnThrProAspHisTyrThrIleuArgIleSerSerIleu 80
DB 321 AGGATATTAAATACTACACAGCCCTGACATTAATCTCTCCGAAATCAGACAGCTTC 380
QY 81 AlaAsnSerPheLeuThrIleIysIysAspLeuArgLeuGlyHisAlaHisMetThrCys 100
DB 381 GCCAATTCCTTCTTACCATCAAGAGACCTCCGCTCTGTCATGACCCACATGACATGAC 440
QY 101 HisCysGlyGluGluAlaMetIysIysTyrSerGlnIleLeuSerHisPheGluIlyLeu 120
DB 441 CATTGTGGGGAGAGCAATGAAATACAGCCGATTCGAGTCACCTTGAAGAGCTG 500
QY 121 GluProGlnAlaAlaValIleValIysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrPhe 140
DB 501 GAACCTCAGGCGACGAGTTGTGAGAGCTTTGGGGAGACTAGACATTTCTTGCAATGATG 560
QY 141 GluGluThrGlu 144
DB 561 GAGGAGACAGAA 572

RESULT 10
ADSI8362
ID ADSI8362 standard; DNA; 926 BP.
AC ADSI8362;
XX
DT 02-DEC-2004 (first entry)
DE Human zcyto10 protein encoding DNA #1.
XX
XX ZCYTO10: cytokine-like polypeptide; cell proliferation;
cell differentiation; autoimmune diseases; diabetes; multiple sclerosis;
rheumatoid arthritis; asthma; psoriasis; cancer; wound; gene therapy;
immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
antiarthritic; antiasthmatic; antipsoriatic; cyostatic; vulnerary;
human; gene; chromosome 1q32.2; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 45..575
FT FT /tag= b
FT FT /product= "Zcyto10 protein"
FT sig_peptide 45..116
FT FT /tag= a
FT mat_peptide 117..572
FT FT /tag= c
FT FT /product= "Mature zcyto10 protein"
XX
XX US2004181040-A1.
XX
XX 16-SEP-2004.
XX
XX 29-DEC-2003; 2003US-00748484.
XX
XX 26-NOV-1997; 97US-0066597.
XX 25-NOV-1998; 98US-00195986.
XX 15-APR-2003; 2003US-00413661.
XX
XX (CONK/) CONKLIN D C.
XX PA (HALD/) HALDEMAN B A.
XX PA (GROS/) GROSSMANN A.
XX
XX Conklin DC, Haldeaman BA, Grosse mann A;
```

```
XX
XX WPI; 2004-667683/65.
XX DR P-PSDB; ADSI8363, ADSI8373.
XX
XX New antibody that selectively binds to a zcyto10 polypeptide useful for
XX modulating cell proliferation, cell differentiation or cytokine
XX production in the prevention or treatment of e.g. autoimmune diseases,
XX cancer or wounds.
XX
XX Disclosure; SEQ ID NO 1; 31pp; English.
XX
XX The present invention relates to a mammalian cytokine-like polypeptide,
XX zcyto10 and its encoding polynucleotide. The invention is useful for
XX modulating cell proliferation, cell differentiation or cytokine
XX production in the prevention or treatment of conditions such as
XX autoimmune diseases (e.g. diabetes, multiple sclerosis, rheumatoid
XX arthritis, asthma or psoriasis) and cancer or wounds. The invention is
XX also useful in gene therapy. The present sequence is the human Zcyto10
XX protein encoding DNA. This zcyto10 gene is located on chromosome 1q32.2.
XX
XX Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1,17e-86 Length: 926
XX Score: 753.00 Matches: 144
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 13 Gaps: 0
XX
XX US-10-789-129-26 (1-144) x ADSI8362 (1-926)
XX
XX 1 CysValIleAlaIarThrAsnLeuGlnIleArgHisGlyPheSerAspIleArgIlySer 20
XX 141 TGTGATGATGCCACAAACCTTCAGGAAATAGAAATGATTTCTGACATACGGGGCAGT 200
XX
XX 21 ValGlnAlaIyAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerIleuGln 40
XX 201 GTGCAGGCCAAGATGAGAAACATTGACATCAGAAATCTTAAGAGAGACTGAGTCTTTCGAA 260
XX
XX 41 AspThrIysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrIleuAsp 60
XX 261 GACACAAAGCCTGGCAATGATGCTGCTCCCTGCGCCATTGCTAAGACTCTATCTTGAC 320
XX
XX 61 ArgValPheIysAsnTyrGlnThrProAspHisTyrThrIleuArgIleSerSerIleu 80
XX 321 AGGATATTAAATACTACACAGCCCTGACATTAATCTCTCCGAAATCAGACAGCTTC 380
XX
XX 81 AlaAsnSerPheLeuThrIleIysIysAspLeuArgLeuGlyHisAlaHisMetThrCys 100
XX 381 GCCAATTCCTTCTTACCATCAAGAGACCTCCGCTCTGTCATGACCCACATGACATGAC 440
XX
XX 101 HisCysGlyGluGluAlaMetIysIysTyrSerGlnIleLeuSerHisPheGluIlyLeu 120
XX 441 CATTGTGGGGAGAGCAATGAAATACAGCCGATTCGAGTCACCTTGAAGAGCTG 500
XX
XX 121 GluProGlnAlaAlaValIleValIysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrPhe 140
XX 501 GAACCTCAGGCGACGAGTTGTGAGAGCTTTGGGGAGACTAGACATTTCTTGCAATGATG 560
XX
XX 141 GluGluThrGlu 144
XX 561 GAGGAGACAGAA 572
XX
XX
XX RESULT 11
XX AEA50048
XX ID AEA50048 standard; cDNA; 926 BP.
XX
XX AEA50048;
XX
XX 11-AUG-2005 (first entry)
XX
XX Full length IL-20 coding sequence.
```

XX ss; gene; Antiinflammatory; Gastrointestinal-Gen.; Antulcer;
 KW Antiarthritic; Dermatological; Antipsoriatic; Antibacterial;
 KW Immunosuppressive; Antimicrobial; IL-Antagonist-20; Interleukin-20;
 KW IL-20; Inflammation; Inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; arthritis; atopic dermatitis; psoriasis; endotoxemia;
 KW septicemia; toxic shock syndrome; infectious disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 45..575
 FT /*tag= a
 PN MO2005052000-A2.
 XX
 PD 09-JUN-2005.
 XX
 PF 19-NOV-2004; 2004MO-US039071.
 XX
 PR 21-NOV-2003; 2003US-0524131P.
 PR 24-MAR-2004; 2004US-0555857P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekhar YA;
 PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
 XX
 DR WPI; 2005-405360/41.
 DR P-PSDB; AEA50049, AEA50050.
 XX
 PT Producing an antibody to an interleukin-20 (IL-20) polypeptide, useful
 PT for treating inflammatory diseases e.g., Crohn's disease, by inoculating
 PT an animal with the polypeptide eliciting an immune response to produce
 PT the antibody.
 XX
 PS Example 1; SEQ ID NO 1; 268bp; English.
 XX
 CC This sequence encodes full length interleukin-20 (IL-20), longer form IL-
 CC 20x1. The method of the invention for producing an antibody to IL-20
 CC comprises inoculating an animal with an IL-20 polypeptide which elicits
 CC an immune response in the animal to produce the antibody, and isolating
 CC the antibody from the animal. The antibody is useful for treating a
 CC pathological condition in a subject associated with IL-20 activity such
 CC as chronic inflammatory condition, specifically inflammatory bowel
 CC disease, ulcerative colitis, Crohn's disease, arthritis, atopic
 CC dermatitis and psoriasis, or acute inflammatory condition such as
 CC endotoxemia, septicemia, toxic shock syndrome and infectious disease. An
 CC antagonist of IL-20 is useful for treating a mammal afflicted with an
 CC inflammatory disease in which IL-20 plays a role such that the
 CC inflammation is reduced, where the antagonist comprises an antibody,
 CC antibody fragment, or binding polypeptide that specifically binds a
 CC polypeptide or polypeptide fragment of IL-20 or a polypeptide or
 CC polypeptide fragment of IL-20, and where the inflammatory activity of IL-
 CC 20 is reduced. The method is useful for producing such therapeutic
 CC antibody. The antibody or antibody fragment, produced using the above
 CC method, binds to IL-20, and inhibits or reduces the pro-inflammatory
 CC activity of IL-20. IL-20-induced proliferation or differentiation of
 CC hematopoietic cells and hematopoietic cell progenitors may be reduced or
 CC inhibited using the antibody.
 XX
 SQ Sequence 926 BP; 258 A; 201 C; 187 G; 280 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.17e-86 Length: 926
 Score: 753.00 Matches: 144
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-789-129-26 (1-144) x AEA50048 (1-926)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
 Db 141 TGTGTATGCGCCGCAAACTTCAGAAATACGAAATGAGATTCTGACATACGGGCAGT 200
 QY 21 ValGlnAlaIleAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
 Db 201 GTCCAGACCCAAAGATGGAATGAAATTCATGACATGAAATCTTAAGAGAGACTGAGTCTTGCA 260
 QY 41 AspThrIleProAlaSerArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
 Db 261 GACACAAAGCGCTCGAATGATGATGCTGCTCGCGCATTTGCTAAGACTTAATCTGGAC 320
 QY 61 ArgValPheIleAsnIleArgIleThrProAspHisIleTyrThrLeuArgGlyIleSerSerLeu 80
 Db 321 AGGGTATTTTAAACATACCAAGACCCCTGACATTAATCTCTCGGAAGATCAGACGCTC 380
 QY 81 AlaSerSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
 Db 381 GCCAATTCCTTCTTACCATCAAGAGAGACCTCGGCTCTGTATCCCAATGACATGACATGC 440
 QY 101 HisCysGlyGluGlnAlaMetIleIleIleIleIleIleIleIleIleIleIleIleIleIle 120
 Db 441 CATTGTGGGAGGAGCAATGAAAGAAATACAGCCAGATTCTGAGTCACTTGAAGAGCTG 500
 QY 121 GluProGlnAlaIleValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 140
 Db 501 GAACCTCAGGCGACGATGTGAAAGCTTTGGGGGAACTGACATTTCTTGTGCAATGAGATG 560
 QY 141 GluIleThrGlu 144
 Db 561 GAGAGACAGAGAA 572
 Db
 RESULT 12
 AEA28786
 ID AEA28786 standard; cDNA; 926 BP.
 XX
 AC AEA28786;
 XX
 DT 11-ANG-2005 (first entry)
 XX
 DE Human interleukin 20 (IL-20) precursor cDNA clone.
 XX
 KW antibody production; cytokine; antiinflammatory; gastrointestinal-gen.;
 KW antulcer; antiarthritic; dermatological; antipsoriatic; antibacterial;
 KW Immunosuppressive; antimicrobial; inflammation; Crohn's disease;
 KW inflammatory bowel disease; ulcerative colitis; cancer; endotoxemia; sepsis;
 KW arthritis; atopic dermatitis; psoriasis; Crohn's disease; IL-20; interleukin-20; ss; gene.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 45..575
 FT /*tag= a
 FT /product= "Human interleukin 20 (IL-20) protein"
 PN MO2005052001-A2.
 XX
 PD 09-JUN-2005.
 XX
 PF 19-NOV-2004; 2004MO-US039097.
 XX
 PR 21-NOV-2003; 2003US-0524131P.
 PR 24-MAR-2004; 2004US-0555857P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Xu W, Kindsvogel WR, Chen Z, Hughes SD, Chandrasekhar YA;
 PI Dillon SR, Lehner JM, Siadak AW, Sivakumar PV, Moore MD;
 XX
 DR WPI; 2005-405360/41.
 DR P-PSDB; AEA28787.
 XX

QY 81 AlaAsnSerPheLeuThrIleValysAspLeuArgLeuCysHisAlaHisMetThrCys 100
 DB 268 GCCAATCTCTTCGACATCAAAAAGACCTGCTGTGTACGCCACATGACCTGC 327
 QY 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
 DB 328 CACTGTGTGAGGAGCAATGAAAAATAACGACGATTCCTGAGCCACTTCGAAAACTG 387
 QY 121 GluProGlnAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
 DB 388 GAACCGGACGACAGTGTGAAAGCTGTGGTGAACGACATTCCTGTGAGTGATG 447
 QY 141 GluGluThrGlu 144
 DB 448 GAGGAGACCGAA 459
 RESULT 14
 AEB26649
 ID AEB26649 standard; DNA; 462 BP.
 AC AEB26649;
 DT 08-SEP-2005 (first entry)
 DE Human interleukin (IL)-20 DNA, SEQ ID NO: 18.
 XX
 KM Expression; gene regulation; toxin; interleukin; gene; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..462
 FT /tag= a
 FT /product= "Human interleukin (IL)-20"
 FT
 PN WO2005058946-A2.
 XX
 PD 30-JUN-2005.
 XX
 PF 10-DEC-2004; 2004WO-US041776.
 XX
 PR 12-DEC-2003; 2003US-0529412P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Chan C, Powder TA;
 XX
 DR MPI; 2005-479318/48.
 DR P-PSDB; AEB26650.
 XX
 PT New Syn 1 and Syn 2 tight regulated synthetic promoters, useful for
 PT controlling uninduced, leaky expression of proteins that are toxic and
 PT interfere with production of recombinant protein from an Escherichia coli
 PT expression system.
 XX
 PS Example 5; SEQ ID NO 18; 39pp; English.
 CC The invention relates to Syn 1 and Syn 2 tight regulated synthetic
 CC promoters and methods for enhancing the expression of recombinant
 CC proteins. The Syn 1 and Syn 2 tight regulated synthetic promoters are
 CC useful for controlling uninduced, leaky expression of proteins that are
 CC toxic and interfere with production of recombinant protein from an
 CC Escherichia coli expression system. They are useful for controlling basal
 CC expression of target genes. The present sequence is the human interleukin
 CC (IL)-20 DNA. This sequence is used in the comparison of promoter
 CC strength.
 SQ Sequence 462 BP; 121 A; 131 C; 117 G; 93 T; 0 U; 0 Other;
 Alignment Scores: 1.38e-86 Length: 462
 Pred. No.: 749.00 Matches: 143
 Score:

Percent Similarity: 100.00%
 Best Local Similarity: 99.31%
 Query Match: 99.47%
 DB: 14
 US-10-789-129-26 (1-144) x AEB26649 (1-462)
 QY 1 CysValIleAlaThrAsnLeuGlnIleArgAsnGlyPheSerAspIleArgLys 20
 DB 28 TGTGTATGCGCCACCACTGCGAGAAATCCGTAACGGTTTCTTGAGATCCGTGCAGC 87
 QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgThrGluSerLeuGln 40
 DB 88 GTCCAGGCCCAAGATGTAACATTGATCCGATCCGTGCTGTCGAGTCTGCGAG 147
 QY 41 AspThrLysProAlaAsnArgCysGlyLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
 DB 148 GACACCCAAACCGCGAACCGTGTGCTGCTGCGCACCTGCTGCTGTATCTGGAC 207
 QY 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgHisLeuSerLeu 80
 DB 208 CGTGTTCGAAAACTACACAGACCCGACACTATACCTGCGTAAATCAGACGCTG 267
 QY 81 AlaAsnSerPheLeuThrIleValysAspLeuArgLeuCysHisAlaHisMetThrCys 100
 DB 268 GCCAATCTCTTCGACATCAAAAAGACCTGCTGTGTACGCCACATGACCTGC 327
 QY 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
 DB 328 CACTGTGTGAGGAGCAATGAAAAATAACGACGATTCCTGAGCCACTTCGAAAACTG 387
 QY 121 GluProGlnAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
 DB 388 GAACCGGACGACAGTGTGAAAGCTGTGGTGAACGACATTCCTGTGAGTGATG 447
 QY 141 GluGluThrGlu 144
 DB 448 GAGGAGACCGAA 459
 RESULT 15
 ABV75154
 ID ABV75154 standard; DNA; 513 BP.
 AC ABV75154;
 DT 19-FEB-2003 (first entry)
 DE EC sequence upstream of IL-20 codon optimised fragment zcyto10X1.
 XX
 KM Protein synthesis; data mining; recombinant; interleukin-20; IL-20;
 KM human; ds.
 OS Synthetic.
 OS Homo sapiens.
 PN WO200283853-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-APR-2002; 2002WO-US011513.
 XX
 PR 13-APR-2001; 2001US-0283688P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Powder TA, Chan C;
 XX
 DR MPI; 2003-067576/06.
 XX
 PT New polynucleotide, useful for producing a nucleic acid construct for
 PT expression of an amino acid sequence of interest.
 PS Example 1; Page 37; 40pp; English.

XX The invention provides a new purified polynucleotide that comprises the
CC nucleic acid sequence A-B-C-D-E; where: A= start codon, B= polynucleotide
CC sequence of 13 nucleic acids, where the sequence has homology with 13
CC base pair (bp) sequence, where at least 5 nucleic acids are identical to
CC a 13 bp sequence (ABV75139), and where the nucleic acid sequence does not
CC code for a stop codon. C= polynucleotide sequence comprising 10, 13, 16
CC or 19 nucleic acids of a 19 bp sequence (ABV75140), D= polynucleotide
CC sequence comprising 8 bp (ABV75141), E= polynucleotide sequence selected
CC from 9 sequences (ABV75144-150) where at least 50% nucleotides are either
CC adenine or thymine, and where only E encodes a stop codon. The
CC polynucleotide is useful for producing a nucleic acid construct for
CC expression of an amino acid sequence of interest. The present sequence
CC represents a sequence comprising an expression cassette (EC)
CC polynucleotide sequence inserted upstream of a human interleukin-20 (IL-
CC 20) codon optimised fragment for expression in E. coli

XX
SQ Sequence 513 BP; 143 A; 145 G; 126 G; 99 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1.61e-86 | Length: | 513 |
| Score: | 749.00 | Matches: | 143 |
| Percent Similarity: | 100.00% | Conservative: | 1 |
| Best Local Similarity: | 99.31% | Mismatches: | 0 |
| Query Match: | 99.47% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |

US-10-789-129-26 (1-144) x ABV75154 (1-513)

| | | | |
|----|-----|---|-----|
| QY | 1 | CyValAlIeAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer | 20 |
| DB | 79 | TGtGTGATCGCCACCAACCTGCAGAAATCCGTAACGGTTCTTGAGATCCGTGCGAC | 138 |
| QY | 21 | ValGlnAlaIysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln | 40 |
| DB | 139 | GTGCAGGCCAAAGATGGTAACATTGACATCCGTATCCGTGCGTACCGAGTCTCTGAC | 198 |
| QY | 41 | AspThrIysProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuIleuAsp | 60 |
| DB | 199 | GACACCAACCGCGGAACCGTGTGCTGCTGCGCCACCTGCGCTGTGTATCTGAC | 258 |
| QY | 61 | ArgValPheIysAsnIleArgIleThrProAspHisIleThrLeuArgIleSerSerLeu | 80 |
| DB | 259 | CGtGTTTCAAAACCTACCAAGACCCGAGCCACTATACCTGCGTAAATCAGCAGCTG | 318 |
| QY | 81 | AlaAsnSerPheLeuThrIleIleIysAspLeuArgLeuCysHisAlaHisMetThrCys | 100 |
| DB | 319 | GCCAACTCCTTCGACCATCAAAAAAGACCTGCGTGTGTACAGCCACATGACCTGC | 378 |
| QY | 101 | HisCysGlyGlnGluAlaMetIleIysIleSerGlnIleLeuSerHisPheGlnIleLeu | 120 |
| DB | 379 | CACGTGTGTGAGAAAGAAATGAAAAATACAGCCAGATTCTGAGCCACTTCGAAAACTG | 438 |
| QY | 121 | GluProGlnAlaIleValIleValIleLeuGlyGlnLeuAspIleLeuLeuGlnIlePheMet | 140 |
| DB | 439 | GAACCGCAGGCGAGAGTGTGTAAGCTGTGTAACGACATTCGTGCAAGTGAATG | 498 |
| QY | 141 | GlnGlnThrGln | 144 |
| DB | 499 | GAGGAGACCGAA | 510 |

Search completed: December 28, 2005, 14:19:32
Job time : 503 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005. CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 28, 2005, 13:52:03 ; Search time 3790 Seconds
(without alignments)
1777.662 Million cell updates/sec

Title: US-10-789-129-26
Perfect score: 753
Sequence: 1 CVIATNQLGIRNGFSDIRG.....AVVKALGELDILLQWMEETE 144

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 2339354128 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame.p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool.p/US10789129/runat.23122005.152720.20276/app_query.fasta_1.327
-DB=EST-QPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNIT9-bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-OCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptlo -NORM=ext -HEADSIZE=500 -MITLEN=0 -MAXLEN=2000000000
-USER=US10789129@CGN_1_1_8010@runat.23122005.152720.20276 -NCPU=6 -ICPU=3
-NO_MMAP -LAEGEUDERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_hic:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_esc7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 749 | 99.5 | 531 | 10 | AY402693 Homo sapi |
| 2 | 603 | 80.1 | 531 | 10 | AY402694 Homo trogl |
| 3 | 565 | 75.0 | 531 | 10 | AY402695 Mus muscu |
| 4 | 547 | 72.6 | 1189 | 4 | AK078698 Mus muscu |
| 5 | 461 | 61.2 | 676 | 2 | BB624019 BB624019 |
| 6 | 328 | 43.6 | 647 | 7 | CR985515 CR985515 |
| 7 | 328 | 43.6 | 695 | 1 | BB064801 BB064801 |

| | | | | | | |
|------|-------|------|------|----|----------|----------|
| 8 | 328 | 43.6 | 699 | 7 | CR992594 | CR992594 |
| c 9 | 275 | 36.5 | 762 | 6 | CA309757 | CA309757 |
| c 10 | 273 | 36.3 | 564 | 6 | BF738279 | BF738279 |
| c 11 | 265 | 35.2 | 748 | 6 | CA306526 | CA306526 |
| 12 | 229 | 30.4 | 709 | 2 | BB639581 | BB639581 |
| c 13 | 228.5 | 30.3 | 897 | 7 | CK800046 | CK800046 |
| c 14 | 217 | 28.8 | 658 | 6 | CD366952 | CD366952 |
| c 15 | 206.5 | 27.4 | 538 | 1 | AM637118 | AM637118 |
| 16 | 206.5 | 27.4 | 703 | 1 | AM635131 | AM635131 |
| 17 | 202.5 | 26.9 | 621 | 11 | DD047027 | DD047027 |
| 18 | 202.5 | 26.9 | 1262 | 4 | CR601530 | CR601530 |
| c 19 | 198.5 | 26.4 | 915 | 1 | AL545939 | AL545939 |
| c 20 | 197.5 | 26.2 | 626 | 6 | CD623370 | CD623370 |
| 21 | 196.5 | 26.1 | 622 | 1 | AM949784 | AM949784 |
| 22 | 190.5 | 25.3 | 763 | 2 | BG189587 | BG189587 |
| 23 | 189.5 | 25.2 | 593 | 1 | AM949792 | AM949792 |
| 24 | 187.5 | 24.9 | 500 | 6 | CB712018 | CB712018 |
| 25 | 173 | 23.0 | 292 | 5 | BX096099 | BX096099 |
| 26 | 166.5 | 22.1 | 1024 | 1 | AL571517 | AL571517 |
| 27 | 151 | 20.1 | 537 | 10 | AY410235 | AY410235 |
| 28 | 149 | 19.8 | 537 | 10 | AY410236 | AY410236 |
| 29 | 145.5 | 19.3 | 727 | 8 | CX789095 | CX789095 |
| 30 | 144 | 19.1 | 537 | 10 | AY410237 | AY410237 |
| 31 | 144 | 19.1 | 590 | 1 | AA607494 | AA607494 |
| 32 | 136 | 18.1 | 585 | 6 | CB442949 | CB442949 |
| 33 | 136 | 18.1 | 619 | 7 | CO259318 | CO259318 |
| 34 | 134 | 17.8 | 337 | 1 | AA344685 | AA344685 |
| 35 | 132 | 17.5 | 534 | 10 | AY410226 | AY410226 |
| 36 | 132 | 17.5 | 666 | 2 | BG538741 | BG538741 |
| 37 | 130.5 | 17.3 | 487 | 9 | AZ224186 | AZ224186 |
| c 38 | 130 | 17.3 | 709 | 9 | BH295670 | BH295670 |
| c 39 | 129 | 17.1 | 1655 | 4 | BC022315 | BC022315 |
| 40 | 127.5 | 16.9 | 478 | 7 | CV025407 | CV025407 |
| 41 | 127 | 16.9 | 534 | 10 | AY410227 | AY410227 |
| c 42 | 125.5 | 16.7 | 629 | 7 | CF896842 | CF896842 |
| c 43 | 118.5 | 15.7 | 778 | 6 | CF127430 | CF127430 |
| 44 | 118 | 15.7 | 317 | 1 | AJ666110 | AJ666110 |
| 45 | 118 | 15.7 | 352 | 1 | AJ668492 | AJ668492 |

ALIGNMENTS

| | | | | | |
|------------|---|------------|-----|--------|-----------------|
| RESULT 1 | AY402693 | 531 bp | DNA | linear | GSS 15-DEC-2003 |
| LOCUS | AY402693 | | | | |
| DEFINITION | Homo sapiens IL20 gene, VIRTUAL TRANSCRIPT, partial sequence, | | | | |
| ACCESSION | AY402693 | | | | |
| VERSION | AY402693.1 | GI:3975676 | | | |
| KEYWORDS | GSS. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | | | |
| | Hominidae; Homo. | | | | |
| REFERENCE | 1 (bases 1 to 531) | | | | |
| AUTHORS | Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A., | | | | |
| | Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., | | | | |
| | Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., | | | | |
| | Adams,M.D. and Cargill,M. | | | | |
| TITLE | Inferring nonneutral evolution from human-chimp-mouse orthologous | | | | |
| | gene trios | | | | |
| JOURNAL | Science 302 (5652), 1960-1963 (2003) | | | | |
| PUBMED | 14671302 | | | | |
| REFERENCE | 2 (bases 1 to 531) | | | | |
| AUTHORS | Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A., | | | | |
| | Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., | | | | |
| | Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., | | | | |
| | Adams,M.D. and Cargill,M. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, | | | | |
| | Rockville, MD 20850, USA | | | | |
| COMMENT | This sequence was made by sequencing genomic exons and ordering | | | | |

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 531)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)

JOURNAL
PUBMED 14671302
2 (bases 1 to 531)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
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ORIGIN
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Pred. No.: 1,41e-59 Length: 531
Score: 565.00 Matches: 109
Percent Similarity: 85.92% Conservative: 13
Best Local Similarity: 76.76% Mismatches: 20
Query Match: 75.03% Indels: 0
Gaps: 0
DB: 10

US-10-789-129-26 (1-144) x AY402695 (1-531)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 97 TGTGGATTACTCGCAAACTTACAGGCAATACAAAGAAATTTCTGAGATTGGGATAGT 156
QY 21 ValGlnAlaYAspGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 157 GTCGACAGCTGAAGATACAAATTTGACATCAGATTTTAAAGACACGACCTGATTGAAA 216
QY 41 AspThrIlePheAlaAsnArgCysCysLeuLeuArgIleLeuLeuArgLeuTyrlleuAsp 60
DB 217 GACATAAAGCTTTTGGATAGGTCGCTCTCTCTCTCATCTGAGATTCTATCTGAGC 276
QY 61 ArgValIlePheIleAsnThrGlnThrProAspHisTyrlThrLeuArgIleSerSerleu 80
DB 277 AGGGATTACAAAGCTTACACAGCCCTGACACCATCCGAGAAAGTACGACGCTC 336
QY 81 AlaAsnSerPheLeuThrIleIleYleYAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 337 GCCAAGCTCTTTCTTATCATCATCAAGAGACCTCTGAGCTGTGCATCTTCACATGCAAGT 396
QY 101 HisCysGlyGluGluAlaMetIleYleYSerGlnIleLeuSerHisPheGluIleu 120
DB 397 CATGTGGGGAAGGACATGAGAAATACCAACCAATTCAGCTCACCTCATAGAGTGG 456
QY 121 GluProGlnAlaIleValIleYleYAlaIleuGlyGluLeuAspIleLeuLeuGlnThrMet 140
DB 457 GAACCTTCAGGCGCGGTGTAAAGGCTTTGGAGAACTAGGCAATCTTCTGAGATGATG 516
QY 141 GluGlu 142
|||||

DB 517 GAGAG 522

RESULT 4
AK078698

LOCUS
DEFINITION
AK078698 1189 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male eyeball cDNA, RIKEN full-length enriched
library, clone:7530415H19 product:interleukin 20, full insert
sequence.

ACCESSION
AK078698
VERSION
AK078698.1 GI:26098048
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636

JOURNAL
PUBMED 10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

JOURNAL
PUBMED 11076861
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sun, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwake, S., Inoue, K., Togawa, K., Izawa, M., Ohara, E., Watanuki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
PUBMED 11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

REFERENCE
AUTHORS 5
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
PUBMED 11076861
6 (bases 1 to 1189)
Adachi, J., Aizawa, K., Akimura, T., Arawaka, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kaukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Satoh, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submision
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Saito-cho, Tsukuba-shi, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome

COMMENT

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

source
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ALIGNMENT SCORES:

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Percent Similarity: 84.62% conservative: 13
Best Local Similarity: 75.52% mismatches: 21
Query Match: 72.64% indels: 1
DB: 4 gaps: 0

US-10-789-129-26 (1-144) x AK078698 (1-1189)

QY 1 CysvalillealathrsanleuginguiilearasnnglyPheSerapllearglyser 20
DB 323 TGTGTATTACTGCAAACTACAGGCAATACAAAGGAATTTCTGAGATTCCGGATTA 382
QY 21 ValGlnAlaLysArgpLyAenlleapllearglleleuArgArgThrGluSerleuGln 40
DB 383 GTCCAAAGCTGAAGATACAAATATTTGACATCAAGATTAAAGACGACTGATCTTTGAAA 442
QY 41 AspThrlyProAlaAsnArgCysCysLeuLeuArgHisleuLeuArgLeuYrleuAsp 60
DB 443 GACATTAAGTCTTTGGATAGGTGCTGCTCTTCGTCATCTAGTGAATTCATCTGGAC 502
QY 61 ArgValPheLysAsnYrGlnThrProAspHisTyrThrleuArgLysIleSerSer-Le 80
DB 503 AGGGTATTCAAAGCTACAGACCCCTGACACATATCCTGAGAAAGATCAAGCCCT 562
QY 80 uAlaenSerPheLeuThrIleLysLysAspLeuArgLeuCyHisAlaHisMetThrCy 100
DB 563 CCCCACTCTTTCTTATCATCAAGAGGACCTCTGCTGTCATCTCAATTCAGATGGCATG 622
QY 100 sHisCysGlyGluGlnAlaMetLysLysYrSerGlnIleLeuSerHisPheGluLysIle 120
DB 623 TCATTGGGGGAAGAACATGGGAATACAAATTCATGAGTCACTTACATAGAGTT 662
QY 120 uGluProGlnAlaAlaValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTrpMe 140
DB 683 GGAACCTTCAAGCGACGGTGGTAAAGCTTTGGAGGAACCTAGGCATTTCTTGAATGAT 742
QY 140 tGluGlu 142
DB 743 GGAGAG 749

RESULT 5
BB624019

LOCUS BB624019 676 bp mRNA linear EST 26-OCT-2001
DEFINITION BB624019 RIKEN full-length enriched, adult male eyeball Mus musculus cDNA clone 7530415H19 5', mRNA sequence.
ACCESSION BB624019
VERSION BB624019.1 GI:16462629
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Komuro,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takehashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

COMMENT

Email: genome-res@gscc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komuro,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtration of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Komuro,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaoka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.
e mouse tissues.

FEATURES

source

1..676
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7530415H19"
/sex="male"
/issue_type="eyeball"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male eyeball"

/note="Site 1: Salt, Site 2: BamHI, cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'
GAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATCTCGAGTTAAATTAATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified phluescript KS(+) after bulk excision
from Lambda FLX I. Cloning sites, 5' end: SalI; 3' end:
BamHI"

ORIGIN

Alignment Scores:

| Pred. No.: | 1,71e-46 | Length: | 676 |
|------------------------|----------|---------------|-----|
| Score: | 461.00 | Matches: | 87 |
| Percent Similarity: | 83.76% | Conservative: | 11 |
| Best Local Similarity: | 74.36% | Mismatches: | 19 |
| Query Match: | 61.22% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-10-789-129-26 (1-144) x B8624019 (1-676)

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QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 319 TGTGTATTACTGCAACACCTACAGGCAATTAAGAAATTTCTGAGATTGGGATAGT 378
QY 21 ValGlnAlaLeuArgGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 379 GTGCAGAGCTGAAGATCAAAATATTGACATCAAGAAATTTAAAGACAGCATGCTTTGAAA 438
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgGlnHisLeuLeuArgLeuTyrLeuAsp 60
DB 439 GACATTAAGCTCTTGGATAGTGTCTCTCTTCGTCATCTAGTCAATTCATTCATTCGAC 498
QY 61 ArgValPheLeuAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSerLeu 80
DB 499 AGGGTATTCAAGCTACACAGACCCCTGACACCAATCCCTGAGAAAGATCAGACAGCTTC 558
QY 81 AlaAsnSerPheLeuThrIleLeuGlyAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 559 GCCAAGCTCTTCTTATCATCAAGAGAGACCTGCTGTCATCTCAGATGCGATGT 618
QY 101 HisCysGlyGlnGlnAlaMetLeuGlyTyrSerGlnIleLeuSerHisPhe 117
DB 619 CATGTGGGGAGAAAGCANTGAGAAATACCAACCAATTCGTGAGTCACTTC 669

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RESULT 6

CR985515

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CR985515 647 bp mRNA linear EST 28-JUN-2005
CR985515 RZPD no. 9016 Homo sapiens cDNA clone RZPD9016M1629 5',
mRNA sequence.
CR985515 GI:68279400
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 647)
Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D.
and Korn, B.
Human T-Lymphocytes library
Unpublished (2005)
Contact: Inge Axlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPD9016M1629.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB No.9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libno=9016 Contact:

Inge Axlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD9016M1629
contact RZPD (product- supporterzpd.de) for further information.
Primer name: qe3_4, Primer sequence: CGGATACAAATCAACACAG.
Location/Qualifiers
1. 647
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD9016M1629"
/issue_type="T-Lymphocytes"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RZPD no.9016"
/note="Vector: pOE80LSN_cloned; Site_1: SalI; Site_2:
NotI; vector:
http://www.rzpd.de/info/vectors/pOE80LSN_cloned.pic.shtml
; 1st strand cDNA was prepared from mRNA obtained from
human T-Lymphocytes with a NotI - oligo(dt) primer [5'
GACTAGTCTAGATCGGAGCGGCCCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to SalI adaptors,
digested with NotI and cloned into the NotI and SalI sites
of the pOE80LSN_cloned vector"

FEATURES

source

Alignment Scores:

| Pred. No.: | 5.58e-30 | Length: | 647 |
|------------------------|----------|---------------|-----|
| Score: | 328.00 | Matches: | 62 |
| Percent Similarity: | 66.20% | Conservative: | 32 |
| Best Local Similarity: | 43.66% | Mismatches: | 48 |
| Query Match: | 43.56% | Indels: | 0 |
| DB: | 7 | Gaps: | 0 |

US-10-789-129-26 (1-144) x CR985515 (1-647)

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QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 122 TGTGTATTACTGCAACACCTACAGGCAATTAAGAAATTTCTGAGATTGGGATAGT 181
QY 21 ValGlnAlaLeuArgGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 182 ATCCAAAGCTAAGACACCTTCCCAATATGCTACTGTCGATTCGACATGGAGACTGCGAG 241
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgGlnHisLeuLeuArgLeuTyrLeuAsp 60
DB 242 ATCATTAAGCTCTTGGATAGTGTCTCTCTTCGTCATCTAGTCAATTCATTCGAC 301
QY 61 ArgValPheLeuAsnTyrGlnThrProAspHisTyrThrLeuArgGlyIleSerSerLeu 80
DB 302 AGGGTATTCAAGCTACACAGACCCCTGACACCAATCCCTGAGAAAGATCAGACAGCTTC 361
QY 81 AlaAsnSerPheLeuThrIleLeuGlyAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 362 GCCAAGCTCTTCTTATCATCAAGAGAGACCTGCTGTCATCTCAGATGCGATGT 421
QY 101 HisCysGlyGlnGlnAlaMetLeuGlyTyrSerGlnIleLeuSerHisPheGlnLeu 120
DB 422 CACTGCAGCAGAGAAAGCCCAAGTCCACAGAGTCAATTCATGACAACTATGATAGCTG 481
QY 121 GtupGlnAlaAlaValAlaValAlaLeuGlnGluLeuAspIleLeuLeuGlnIlePheMet 140
DB 482 GAGGTCCAGCGTCTGCGCATTAATTCCTGGAGAGCTCGAGGTCTTTCTAGCCCTGAGTT 541
QY 141 Gtuglu 142
DB 542 AATAAG 547

```



```

/notes="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGGAGAGAGATTCGAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGCTTCGAGCTAAATTAATTAATTCCTCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda PLC I. Cloning sites, 5' end: Sali, 3' end:
BamHI"

ORIGIN

Alignment Scores:
Pred. No.:
Score: 6.17e-30 Length: 695
Percent Similarity: 328.00 Matches: 68
Best Local Similarity: 88.24% Conservative: 7
Query Match: 80.00% Mismatches: 10
DB: 43.56% Indels: 1
Gaps: 0

US-10-789-129-26 (1-144) x BB064801 (1-695)

QY 58 TyleuAspArgValPheIysAenTYGIntHrProAspHisTYrThrIeuArgIyle 77
Db 3 TATCTGGACAGGGGTATTCAAAGTCTACCAAGACCCCTGACCCCATCTCCGAGAAAGATC 62
78 SerSerIeuAlaAsnSerPheIeuThrIleIysIeAspIeuArgIeuCysHisAlaHis 97
Db 63 AGCAGCCTCGCCCAATTCCTTTCTTATCATCAAGAAGACCTTCACAGCTGTCAATTCAC 122
98 MetThrCysHisIcCysGcIyGluIuAlaMeIyIsTYSerGlnIleIeuSerHisPhe 117
Db 123 ATGGCAGTGTCA-TGTGGGGAAGAAGCAATGAGAAATACCAACAAATTCGTAGTCACCTC 181
QY 118 GluIyIeIeuGluProGlnAlaAlaValIyAlaIeIeuGlyIuIeuAspIleIeuIeu 137
Db 182 ATGAGAGTTGGAACCTTCACGCGAGCGGTGTAAAGCTTTGGGAGAACTGACATTCCTG 241
QY 138 GluTrpMetGluIu 142
Db 242 AGATGATGAGAGAG 256

RESULT 8
CR992594 699 bp mRNA linear EST 28-JUN-2005
LOCUS CR992594
DEFINITION CR992594 RZPD no.9016 Homo sapiens cDNA clone RZPDp9016L545 5',
mRNA sequence.
ACCESSION CR992594
VERSION CR992594.1 GI:68286479
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 699)
Heil,O., Ebert,L., Hennig,S., Henze,S., Redelof,U., Schneider,D.
and Korn,B.
Human T-Lymphocytes library
Unpublished (2005)
Contact: Inge Arlt
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.tzpd.de

```


RZPD; RZPDp9016C1545.
 RZPDLib; (Human T-Lymphocytes) RZPD Lib No.9016
 http://www.rzpd.de/cgi-bin/products/set.cgi?libno=9016 Contact:
 Inge Ariart
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 100
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available from RZPD;
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=RZPDp9016C1545
 contact RZPD (product support@rzpd.de) for further information.
 Primer name: qe3_4, primer sequence: CGATTAACAATTACACAG.

FEATURES

source
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 /db_xref="taxon:9606"
 /clone="RZPDp9016C1545"
 /tissue_type="T-Lymphocytes"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="RZPD no.9016"
 /note="Vector: pQE80LSN_cloned; site_1: SalI; site_2:
 NotI; vector:
 http://www.rzpd.de/info/vectors/pQE80LSN_cloned.pic.shtml
 ; 1st strand cDNA was prepared from mRNA obtained from
 human T-Lymphocytes with a NotI - oligo(dT) primer [5']
 GACTGTTTAAATCGACGCGCGCCCTTTTCTTTTCTTTT 3'].
 Double-stranded cDNA was ligated to SalI adaptor,
 digested with NotI and cloned into the NotI and SalI sites
 of the pQE80LSN_cloned vector"

ORIGIN

Alignment Scores:

Pred. No.: 6,22e-30 Length: 699
 Score: 328.00 Matches: 62
 Percent Similarity: 66.20% Conservative: 32
 Best Local Similarity: 43.66% Mismatches: 48
 Query Match: 43.56% Indels: 0
 DB: 7 Gaps: 0

US-10-789-129-26 (1-144) x CR992594 (1-699)

QY 1 CysValIleAlaLeuThrAsnLeuGlnIleArgAsnGlyPheSerAspIleArgGlySer 20
 DB 128 TGTCTGATTTCCACGACATGACCATATATGAAAGAGTTTCCAGAAATTCAGAGAGCC 187
 QY 21 ValGlnAlaLeuAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
 DB 188 ATCCAAAGCTAAGAGACCTTCCCAATGTCATATCTCTCCACATGGAGACTCTGCAG 247
 QY 41 AspThrLySPALaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrlleuAsp 60
 DB 248 ATCATTAAGCCCTTGATGTGTGCTGCGTACCAAGAACCTCTGCGCTTACACGAGAC 307
 QY 61 ArgValPheLeuAsnTyrlThrProAspHisTyrlThrLeuArgTyrlleuSerLeu 80
 DB 308 AGCGTGTTCAGATCATGAGAGCCCAATCTTGAAGAAATTCAGAAATTCAGAGCATY 367
 QY 81 AlaAsnSerPheLeuThrIleLeuLyAspLeuArgLeuGlyHisIleHisMetThrCys 100
 DB 368 GCCAACTCTTCTCTACATGCGAAGAACTCTGCGGCAATGTCAGGAACAGAGGAGTGT 427
 QY 101 HisGlyGlnGlnAlaMetLySlyTyrlSerGlnIleLeuSerHisPheGlnIleu 120
 DB 428 CACTGACGAGGAGGAGGACCAATGCGACAGAGTCAATGACCAATATGATGACGCTG 487
 QY 121 GluProGlnAlaAlaValValysAlaLeuGlyGlnLeuAspIleLeuLeuGlnIlePhe 140
 DB 488 GAGGTTCACGCTGCGCATTAATCTCTGGAGAGCTGACGCTTCTTACCTTGATTT 547
 QY 141 GluGln 142

DB 548 AATAAG 553

...

RESULT 9
 CA309757/c
 LOCUS
 DEFINITION
 UI-H-FT1-bic-n-07-0-UI.g1 NCI CGAP FT1 Homo sapiens cDNA clone
 UI-H-FT1-bic-n-07-0-UI 3', mRNA sequence.
 CA309757
 CA309757.1 GI:24472811
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo
 1 (bases 1 to 762)
 NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@iowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.
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 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-bic-n-07-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP_FT1"
 /note="Organ: Lung; Vector: pRT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP FT1 is a normalized cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The RNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
 (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3
 hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lemon and Soares, Genome
 Research, 6:791-806, 1996. First strand cDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded cDNA was ligated to an EcoR I adaptor,
 digested with Not I, and cloned directionally into
 pRT73-Pac vector. The oligonucleotide used to prime the
 synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (drr)18 tail. The sequence tag for this library is
 GGCATGCGG. The tissue was provided by Dr. Gary W.
 Hunninghake of the University of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage


```

/clone="UI-H-FT1-bhw-m-10-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP FT1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP FT1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldi, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT73-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(GT)18 tail. The sequence tag for this library is
GGCGATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCGATGCCG"

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ORIGIN

```

Alignment Scores:
Pred. No.: 4,69e-22 Length: 748
Score: 265.00 Matches: 51
Percent Similarity: 65.79% Conservative: 24
Best Local Similarity: 44.74% Mismatches: 39
Query Match: 35.19% Indels: 0
DB: 6 Gaps: 0

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US-10-789-129-26 (1-144) x CAJ06526 (1-748)

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QY 29 AapIleArgIIleuArgArghrGluSerIleuAlaSerThrIleProlaIaenArgCys 48
DB 744 AATGTACTATCTCTGACACATTTGAGACTCTGACATCATTAAGCCCTTAACTGTGTC 685
QY 49 CysLeuLeuArgHisIleuLeuArgLeuTyrIleuAspArgValPheIysAsnTyrGlnThr 68
DB 684 TGGGTACCAAGAACTCTCTGGCTTCTACGTGGACAGGGGTGCANAGATCTACGAGAG 625
QY 69 ProAspHisTyrThrIleuArgIlysIleSerSerIleuAlaAsnSerPheLeuThrIleLys 88
DB 624 CCAAAACCCCAAAATCTTGAAGAAAATACACAGATTCACCACTCTTCTTAAACATGACG 565
QY 89 LysAspIleuArgLeuCysHisAlaHisMetThrCysHisCysGlyGluGluAlaMetLys 108
DB 564 AAAAAGCTTCGGCAAGTTCAGAAACAGAGCAAGTGTCACTGCACGAGAGAAAGCAACCAAT 505
QY 109 LysTyrSerGlnIleuSerHisPheGluLysLeuGluProGlnAlaIaIaValLys 128
DB 504 GCCACACAGATCATCATGACAACTATGATCTACGTGAGAGTCCACCTCTGCAATTAA 445
QY 129 AlaLeuGlyIleuAspIleuLeuGlnTyrMetGluGlu 142
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DB 444 TCCCTGGAGAGCTGACGCTTTCTTACGCTGATTAAATAG 403
RESULT 12
BB639581
LOCUS BB639581 709 bp mRNA linear EST 26-OCT-2001
DEFINITION BB639581 RIKEN full-length enriched, 7 days neonate cerebellum Mus
musculus cDNA clone A730059E15 5', mRNA sequence.
ACCESSION BB639581
VERSION BB639581.1 GI:16474967
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 709)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J.,
Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshitake Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsura,S., Kawai,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1571-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamana,K.I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
location/Qualifiers
1..709
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A730059E15"
/tissue_type="cerebellum"
/dev_stage="7 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 7 days neonate
cerebellum"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in

```

FEATURES

source

RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 5' GAGAGAGAGAGATCCAGAGCTTTTCTTTTCTTTTNN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence 5' GAGAGAGAGATCTCGAGTTAATTAATATCCCCCCCC 3'. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLX I."

ORIGIN

Alignment Scores:

| | | | |
|------------------------|---------|---------------|-----|
| Pred. No.: | 1,3e-17 | Length: | 709 |
| Score: | 229.00 | Matches: | 46 |
| Percent Similarity: | 63.30% | Conservative: | 23 |
| Best Local Similarity: | 42.20% | Mismatches: | 38 |
| Query Match: | 30.41% | Indels: | 2 |
| DB: | 2 | Gaps: | 1 |

US-10-789-129-26 (1-144) x BB639581 (1-709)

```
QY 35 ArgThGluSerLeuGlnAepThr-----LysProAlaAenArgCysCysLeuLeuArg 52
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 33 AGGACTCTGCTGGAGGAGACACCGAGAGAGCTGGAGATGTGCTGCATGACCCAC 92
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 53 HisLeuLeuArgLeuTyrlLeuAspArgValPheLysAenTyrlGlnThrProAepHisTyR 72
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 93 AACCTGCTGACATTCATCAAGACAGGAGTGTCCAGACCACTCGAGAGAGACCTTGAG 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 73 ThrLeuArgLysIleSerSerLeuAlaAenSerPheLeuThrIleLysLysAspLeuArg 92
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 153 GCTTAAAGAGAAATCAGCAGCATTCGCCACTCTTCTCGCGGAGAGAAATCTCTGAG 212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 93 LeuCyHisAlaHisMetThrCysHisCysGlyGluGluAlaMetLysLysTyRserGln 112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 213 CGATGTCAGGTGACAGACACATGTAACTGACAGTCAGAGACCAATGCACTAGGATC 272
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 113 IleLeuSerHisPheGluLysLeuGluProGlnAlaAlaValLysLysAlaLeuGlu 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 273 ATCATGACACACTCAATCAATCAGCTGAGAGCTCTCATCTCTGCTTAAAGTCTTAAAGAGA 332
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 133 LeuAspIleLeuLeuGlnIntyPmetGlu 141
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 333 CTGAACATACCTTTTAAAGCTGGATTGAC 359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 13

CR800046 897 bp mRNA linear EST 25-FEB-2004
LOCUS AGENCOURT 18791077 NICHD_XGC_Te2N Xenopus laevis cDNA clone
DEFINITION IMAGE:7203819 5', mRNA sequence.

ACCESSION CR800046
VERSION CR800046
KEYWORDS GI:42812042

SOURCE EST.
ORGANISM Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 897)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-remail.nih.gov
Tissue Procurement: Igor B. David
cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Data distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM15082 row: e column: 01
High quality sequence stop: 750.

FEATURES

source

1..897 location/Qualifiers

/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:7203819"
/tissue_type="Pooled samples from 6 adult male testis"
/lab_host="DH10B Tona"
/clone_11b="NICHD_XGC_Te2N"
/note="Organ: testis; Vector: pExpress-1; Site 1: EcoRV,
Site 2: NotI; RNA obtained from 6 adult male testis. cDNA
was primed using oligo-dT primer:
5'-pACTAGTCTAGATGCGAGCGGCCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1kb
resulted in an average insert size of 1.15 kb. This
primary, microquantified library is normalized to Cots
(non-normalized primary library is NICHD_XGC_Te2) and was
constructed by Express Genomics (Frederick, MD). Note:
this is an NIH_XGC library"

ORIGIN

Alignment Scores:

| | | | |
|------------------------|---------|---------------|-----|
| Pred. No.: | 2,1e-17 | Length: | 897 |
| Score: | 228.50 | Matches: | 42 |
| Percent Similarity: | 57.75% | Conservative: | 40 |
| Best Local Similarity: | 29.58% | Mismatches: | 59 |
| Query Match: | 30.35% | Indels: | 1 |
| DB: | 7 | Gaps: | 1 |

US-10-789-129-26 (1-144) x CR800046 (1-897)

```
QY 1 CysValIleAlaThrAenLeuGlnGluIleArgAenGlyPheSerAepIleArgGlySer 20
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 294 TGCCCTGTGCTCTTGGATATCCAGAGGTTTAAATAATACATGAGTCTGCAAGAGGTC 353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 21 ValGlnAlaLysAspLysAenIleAepIleArgIleLeuArgArgThrGlnSerLeuGln 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 354 TTGCACAAAGAAGATGTGATTACAGATGTGAGCCTCTG--AAACCCAAAGCTGGAAT 410
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 41 AepThrLysProAlaAenArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrlLeuAsp 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 411 CAGATACATGCATCTGAGCAAGCTGCTCTCTTCAAACTGGAGCTTTTATCATGAAAC 470
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ArgValPheLysAenTyrlGlnThrProAepHisTyRThrLeuArgLysIleSerLeu 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 471 AATATTTCCTCCAAACTGGAAATCTCTCAATTAAAGACAGAAAGTCTTATCATTTTA 530
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 AlaAenSerPheLeuThrIleLysLysAspLeuArgLeuCyHisAlaHisMetThrCys 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 531 GCTAACTGTGCTCTGGGCTTAAAGATAGAGCTCAGCATTCATCTCTTATGAGGTAT 590
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 101 HisCysGlyGluGluAlaMetLysLysTyRserGlnIleLeuSerHisPheGluLysLeu 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 591 CCTGTGCGATGATGACACACAAATTAATGAAGACTTTAAGGAACCTTTTACAGATG 650
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 GluProGlnAlaAlaValLysLysAlaLeuGluGluLeuAspIleLeuLeuGlnIntyPmet 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 651 GAGACAGAGACAGCTATTATTAAAGCTATTGAGACTGAATATCTGATTCGCTGGTTG 710
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 141 GluGlu 142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 711 GAAAAA 716
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 14

CD366952/c 658 bp mRNA linear EST 05-AUG-2004
LOCUS CD366952

| | |
|------------|--|
| DEFINITION | UI-H-FT2-bj-p-1-22-0-UI_s1 NCI CGAP FT2 Homo sapiens CDNA clone |
| ACCESSION | CD366952 |
| VERSION | CD366952.1 |
| KEYWORDS | EST. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo. |
| REFERENCE | 1 (bases 1 to 658) |
| AUTHORS | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . |
| TITLE | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index |
| JOURNAL | Unpublished (1997) |
| COMMENT | Contact: Robert Stransberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Gary W. Humnphake, U of I CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html Seq primer: M13 FORWARD POLYA=Yes. |
| FEATURES | Location/Qualifiers |
| SOURCE | 1..658 |

TAG_SEQ=GGCCATGCCG"

```

Alignment Scores:
Pred. No.:      3,65e-16      length: 658
Score:          217.00      Matches: 41
Percent Similarity: 68.24      Conservative: 17
Best local Similarity: 48.24      Mismatches: 27
Query Match:    28.82%      Indels: 0
DB:              6      Gaps: 0
US-10-789-129-26 (1-144) x CD36952 (1-658)

```

US-10-789-129-26 (1-144) x CD366952 (1-658)

| | | | | |
|------------|--|---|---|-----------------------------|
| Oy | | 58 | TtyleunspayvalplelyasnyrcimhrProapsh:eryrThleuArygysile | 77 |
| Db | | 657 | TACGTGACAGCGGTTCATCAGATCATCAGAGCCAAACCCTTGAAGAAAATC | 598 |
| Oy | | 78 | SerSerleualaanserPheLeuthrlleylsyAspleuArygleuCyshtalahlis | 97 |
| Db | | 597 | AGGACGATTCGCCACTCTTTCTCTTACATGCAGAAACTCTGGCGCAATGTCAGAGAONG | 538 |
| Oy | | 98 | MethrcCyshhsGsyglYguJualAmetylslsYrsargInlleuSerhsiphe | 117 |
| Db | | 537 | AGGACGTGTCACTCAGCGAGGAAAGCCCAATGCCACAGATCATCATGACAATAT | 478 |
| Oy | | 118 | GltutylsleugluPrOglnalaaValysAlaleuGlYguJleuAspIleuenu | 137 |
| Db | | 477 | GATCAGCGTGAGGATTCACGCGTCTGCCATTAAATCCCTGGGAGAGCTGAGGTCTTTCTTA | 418 |
| Oy | | 138 | GIntpmetcluguJu | 142 |
| Db | | 417 | GCCTGATTAATAAG | 403 |
| RESULT 15 | | | | |
| LOCUS | | AM637118 | 538 bp | mRNA linear EST 26-APR-2001 |
| DEFINITION | | B154f02.v1 Blackshear/Soates normalized Xenopus egg library | Xenopus | egg |
| ACCESSION | | AM637118 | | |
| VERSION | | AM637118.1 | GI:7394220 | EST. |
| KEYWORDS | | | | |
| SOURCE | | | Xenopus laevis (African clawed frog) | |
| ORGANISM | | | Xenopus laevis | |
| | | | Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| | | | Ampiphilia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; | |
| | | | Xenopodinae; Xenopus; Xenopus. | |
| | | | 1 (bases 1 to 538) | |
| REFERENCE | | | Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G. | |
| AUTHORS | | | Jr., Moore,D.T., Boultard,G.G., Beckstrom-Sternberg,S.M., | |
| | | | Touchman,J.W., Bonaldo,M.F. and Soates,M.B. | |
| | | | The NIHES Xenopus maternal EST project: interim analysis of the | |
| | | | first 13,879 ESTs from unfertilized eggs | |
| | | | Gene 267 (1), 71-87 (2001) | |
| JOURNAL | | | 11311557 | |
| PUBMED | | | | |
| COMMENT | | | Contact: Perry J. Blackshear | |
| | | | Office of Clinical Research and Laboratory of Signal Transduction | |
| | | | National Institute of Environmental Health Sciences | |
| | | | A2-05 NIHES, 101 Alexander Drive, Research Triangle Park, NC 27709, | |
| | | | USA | |
| | | | Tel.: 919 541-4899 | |
| | | | Fax: 919 541-4571 | |
| | | | Email: black009@niehs.nih.gov | |
| | | | Cclone is available through Research Genetics, Inc., 2130 Memorial | |
| | | | Parkway, Huntsville, AL 35901 | |
| | | | phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email | |
| | | | chnae@egen.com | |
| | | | DNA Sequencing and analyses performed by National Institutes of | |
| | | | Health Intramural Sequencing Center (NISC). | |
| | | | PCR Primers | |
| | | | FORWARD: TGTAAACGACGGCCAGT | |
| | | | BACKWARD: CAGGAACGATATGAC | |
| | | | Plate: 0054 row: F column: 02 | |
| | | | Seq primer: T7 primer | |
| FEATURES | | | Location/Qualifiers | |
| SOURCE | | | 1..538 | |

```

source
1..538
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="PBX0054P02"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/clone_lib="Blackshear/Soares normalized Xenopus egg"

```

```
/clone_11b="Blackshear/Soares normalized Xenopus egg
```

library"
 /note="vector: pT73-Pac; Site_1: EcoRI; Site_2: NotI;
 PolyA-selected mRNA was prepared from unfertilized Xenopus
 laevis eggs. The library was constructed in the vector
 pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
 Soares, M.B. 'Normalization and subtraction: two
 approaches to facilitate gene discovery', Genome Research
 6:791-806, 1996. The first strand synthesis used a
 NotI-dT18 primer; double stranded cDNAs were ligated to
 EcoRI adapters, digested with NotI, and directionally
 cloned into the NotI and EcoRI-digested pT73-Pac vector.
 The library contained approximately 7.2×10^5
 recombinants, with average insert sizes of 1-1.5 kb."

ORIGIN

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 5.55e-15 | Length: | 538 |
| Score: | 206.50 | Matches: | 39 |
| Percent Similarity: | 59.66% | Conservative: | 32 |
| Best Local Similarity: | 32.77% | Mismatches: | 47 |
| Query Match: | 27.42% | Indels: | 1 |
| DB: | 1 | Gaps: | 1 |

US-10-789-129-26 (1-144) x AW637118 (1-538)

```

QY      24  LysAspGClYAsnIleAepIleAArgIleLeuAArgThrGluSerLeuGlnAepThrIys 43
      |||||  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
DB      85  AAGGATGTGATTACAGATGTCAGCCTCTG--AAAGCCAAAGTGCTGAATCAGATACAT 141

QY      44  ProAlaAsnArgCysCysLeuLeuAArgHisIleuLeuAArgLeuTyrLeuAAspArgValPhe 63
      |||||  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
DB     142  CCACTGAGCAATGCTCTCTCTTCAAACTGGAGCGTTTTCATGAAACAATATTTC 201

QY      64  LysAsnTyrGlnThrProAspHisTyrThrLeuAArgIleSerSerLeuAlaAsnSer 83
      ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
DB     202  CCAAACTGGAAATCTCTTCAATTAAGGACGAGAAAGGCTTAAATCATTTAGCTAACTCT 261

QY      84  PheLeuThrIleIyAspLeuAArgLeuCysHisAlaHisMetThrCysHisCysGly 103
      |||||  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
DB     262  GTCCTGGGTCTAAAGATAGAGCTCAAGCATTTGCTATGAGGTGCCCTGTGGT 321

QY     104  GluGluAlaMetLysLysTyrSerGlnIleuSerHisPheGluLysLeuGlnProGln 123
      ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
DB     322  GATCAGTCACACAAATATTAGAAAGACTTTAGGGAACCTTTTACCGATGAGACAGAA 381

QY     124  AlaAlaValValIysAlaLeuGlyGluLeuAspIleLeuLeuGlnITPMeGluGln 142
      |||||  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
DB     382  GCAGCTATTATTAAAGCTATTGAGACTGAATATCTGATGCGTGTGGAATAA 438

```

Search completed: December 28, 2005, 16:12:12
 Job time : 3796 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 28, 2005, 14:19:09 ; Search time 820 Seconds
(without alignments)
1452.183 Million cell updates/sec

Title: US-10-789-129-26
Perfect score: 753
Sequence: 1 CVIATNQBIRNGFSDIRGS.....AVKALGELDILLQWMEETE 144

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlp
-MODEL=frame.p2n.model -DEVT=xlp
-O=/cgn2_1/USPTO_spool_p/US10789129/runat_23122005_152721_20318/app_query.fasta_1.327
-DB=Published Applications NA_Main -QFMT=fastap -SUFFIX=p2n.rmpbm
-MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1
-MATRIX=bloum62 -TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALLEN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext
-HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10789129@cgn_1.1.1549@runat_23122005_152721_20318 -NCFU=6 -ICPU=3
-NO_MMAP -LARGEBUQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 753 | 100.0 | 926 | 6 | US-10-321-163-1 |
| 2 | 753 | 100.0 | 926 | 6 | US-10-413-661-1 |
| 3 | 753 | 100.0 | 926 | 6 | US-10-172-118-186 |
| 4 | 753 | 100.0 | 926 | 7 | US-10-342-887-186 |
| 5 | 753 | 100.0 | 926 | 7 | US-10-789-129-1 |
| 6 | 753 | 100.0 | 926 | 7 | US-10-789-251-1 |
| 7 | 753 | 100.0 | 926 | 7 | US-10-789-968-1 |

| | | | | | | |
|----|-----|-------|------|---|-------------------|--------------------|
| 8 | 753 | 100.0 | 926 | 8 | US-10-748-484-1 | Sequence 1, Appli |
| 9 | 753 | 100.0 | 926 | 9 | US-10-994-116-1 | Sequence 1, Appli |
| 10 | 753 | 100.0 | 926 | 9 | US-10-994-151-1 | Sequence 1, Appli |
| 11 | 749 | 99.5 | 462 | 6 | US-10-122-882B-14 | Sequence 14, Appli |
| 12 | 749 | 99.5 | 462 | 6 | US-11-054-063-18 | Sequence 18, Appli |
| 13 | 749 | 99.5 | 513 | 6 | US-10-122-882B-17 | Sequence 17, Appli |
| 14 | 749 | 99.5 | 867 | 7 | US-10-467-431-1 | Sequence 1, Appli |
| 15 | 749 | 99.5 | 867 | 7 | US-10-466-699A-1 | Sequence 1, Appli |
| 16 | 746 | 99.1 | 926 | 8 | US-10-807-837-7 | Sequence 7, Appli |
| 17 | 739 | 98.1 | 1571 | 3 | US-09-946-374-401 | Sequence 401, App |
| 18 | 739 | 98.1 | 1571 | 3 | US-10-006-867-137 | Sequence 137, App |
| 19 | 739 | 98.1 | 1571 | 3 | US-10-052-586-609 | Sequence 609, App |
| 20 | 739 | 98.1 | 1571 | 5 | US-10-063-547-137 | Sequence 137, App |
| 21 | 739 | 98.1 | 1571 | 5 | US-10-063-551-137 | Sequence 137, App |
| 22 | 739 | 98.1 | 1571 | 5 | US-10-028-072-97 | Sequence 97, Appli |
| 23 | 739 | 98.1 | 1571 | 5 | US-10-028-072-545 | Sequence 545, App |
| 24 | 739 | 98.1 | 1571 | 5 | US-10-174-590-609 | Sequence 609, App |
| 25 | 739 | 98.1 | 1571 | 5 | US-10-176-758-609 | Sequence 609, App |
| 26 | 739 | 98.1 | 1571 | 5 | US-10-175-737-609 | Sequence 609, App |
| 27 | 739 | 98.1 | 1571 | 5 | US-10-063-616-137 | Sequence 137, App |
| 28 | 739 | 98.1 | 1571 | 5 | US-10-174-581-609 | Sequence 609, App |
| 29 | 739 | 98.1 | 1571 | 5 | US-10-176-483-609 | Sequence 609, App |
| 30 | 739 | 98.1 | 1571 | 5 | US-10-176-749-609 | Sequence 609, App |
| 31 | 739 | 98.1 | 1571 | 5 | US-10-176-914-609 | Sequence 609, App |
| 32 | 739 | 98.1 | 1571 | 5 | US-10-176-915-609 | Sequence 609, App |
| 33 | 739 | 98.1 | 1571 | 5 | US-10-140-808-97 | Sequence 97, Appli |
| 34 | 739 | 98.1 | 1571 | 5 | US-10-140-808-545 | Sequence 545, App |
| 35 | 739 | 98.1 | 1571 | 5 | US-10-063-569-137 | Sequence 137, App |
| 36 | 739 | 98.1 | 1571 | 5 | US-10-063-513-137 | Sequence 137, App |
| 37 | 739 | 98.1 | 1571 | 5 | US-10-063-515-137 | Sequence 137, App |
| 38 | 739 | 98.1 | 1571 | 5 | US-10-063-512-137 | Sequence 137, App |
| 39 | 739 | 98.1 | 1571 | 5 | US-10-121-049-97 | Sequence 97, Appli |
| 40 | 739 | 98.1 | 1571 | 5 | US-10-121-049-545 | Sequence 545, App |
| 41 | 739 | 98.1 | 1571 | 5 | US-10-173-706-609 | Sequence 609, App |
| 42 | 739 | 98.1 | 1571 | 5 | US-10-175-738-609 | Sequence 609, App |
| 43 | 739 | 98.1 | 1571 | 5 | US-10-175-752-609 | Sequence 609, App |
| 44 | 739 | 98.1 | 1571 | 5 | US-10-176-482-609 | Sequence 609, App |
| 45 | 739 | 98.1 | 1571 | 5 | US-10-176-757-609 | Sequence 609, App |

ALIGNMENTS

RESULT 1
US-10-321-163-1
; Sequence 1, Application US/10321163
; Publication No. US2003016181A1
; GENERAL INFORMATION:
; APPLICANT: Chandrasekhar, Yasmin
; APPLICANT: McKernan, Patricia
; TITLE OF INVENTION: METHOD FOR TREATING CERVICAL CANCER
; FILE REFERENCE: 01-44US
; CURRENT APPLICATION NUMBER: US/10/321,163
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 60/341,783
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45) ... (572)
US-10-321-163-1

Alignment Scores:
Pred. No.: 8.29e-93
Score: 753.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6
Caps: 0

Length: 926
Matches: 144
Conservative: 0
Mismatch: 0
Indels: 0
Caps: 0

US-10-789-129-26 (1-144) x US-10-321-163-1 (1-926)

```
QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTATGCGCCAAACCTTCAGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaIleAsnArgGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 201 GTGCAGAGCCAAAGATGAAACATTGACATCAATCTTAAAGAGAGACTGAGTCTTTGCAA 260
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCCTCGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320
QY ArgValPheIleAsnArgIleThrProAspHisTyrThrLeuArgIleSerSerLeu 80
DB 321 AGGGTATTTAAACCTACCAAGACCCCTGACCATTAATCTCTCCGGAAGATCAGCAGCTTC 380
QY AlaAsnSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
DB 381 GCCAATTCTCTTCTTCAATCAAGAGACCTCCGGCTCTGTCATGCCCATGACATGTC 440
QY HisCysGluGluGluAlaIleValIleValIleValIleValIleValIleValIleValIle 120
DB 441 CATTGTGGGAGAGAGCAATGAAATACAGCAGATCTTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGlnAlaIleValIleValIleValIleValIleValIleValIleValIleValIle 140
DB 501 GAACCTCAGGCAAGTGTGAAAGGCTTTGGGGAACTAGACATTTCTTGCATGAGATG 560
QY 141 GluGluThrGlu 144
DB 561 GAGGAGACAGAA 572
```

RESULT 2

```
US-10-413-661-1
; Sequence 1, Application US/10413661
; Publication No. US20030176657A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Haldeman, Betty A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/413,661
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/199,586
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,597
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)....(572)
US-10-413-661-1
```

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 8,296-93 | Length: | 926 |
| Score: | 753.00 | Matches: | 144 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-10-789-129-26 (1-144) x US-10-413-661-1 (1-926)

```
QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTATGCGCCAAACCTTCAGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200
```

DB 141 TGTGTATGCGCCAAACCTTCAGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200

```
QY 21 ValGlnAlaIleAsnArgGlyAsnIleAspIleArgIleLeuArgArgThrGluSerLeuGln 40
DB 201 GTGCAGAGCCAAAGATGAAACATTGACATCAATCTTAAAGAGAGACTGAGTCTTTGCAA 260
QY 41 AspThrIleProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCCTCGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320
QY ArgValPheIleAsnArgIleThrProAspHisTyrThrLeuArgIleSerSerLeu 80
DB 321 AGGGTATTTAAACCTACCAAGACCCCTGACCATTAATCTCTCCGGAAGATCAGCAGCTTC 380
QY AlaAsnSerPheLeuThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100
DB 381 GCCAATTCTCTTCTTCAATCAAGAGACCTCCGGCTCTGTCATGCCCATGACATGTC 440
QY HisCysGluGluGluAlaIleValIleValIleValIleValIleValIleValIleValIle 120
DB 441 CATTGTGGGAGAGAGCAATGAAATACAGCAGATCTTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGlnAlaIleValIleValIleValIleValIleValIleValIleValIleValIle 140
DB 501 GAACCTCAGGCAAGTGTGAAAGGCTTTGGGGAACTAGACATTTCTTGCATGAGATG 560
QY 141 GluGluThrGlu 144
DB 561 GAGGAGACAGAA 572
```

RESULT 3

```
US-10-172-118-186
; Sequence 186, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 186
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF224266
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-186
```

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 8,296-93 | Length: | 926 |
| Score: | 753.00 | Matches: | 144 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-10-789-129-26 (1-144) x US-10-172-118-186 (1-926)

```
QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTATGCGCCAAACCTTCAGAAATACGAAATGGATTTTCTGACATACGGGGCAGT 200
```


QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB GTGCAAGCCAAAGATGGAAACATTGACATCAGAACTTAAGAGAGACTGAGCTTTGCAA 260
QY 41 AspThrLysProAlaAsnArgCysCysGluLeuArgHisGluLeuArgLeuTyrLeuAsp 60
DB GACACAAAGCTCGCAATGATGATGCTGCTCCGCGCAATTTGCTAAGACTCTATCGGAC 320
QY 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB AGGATTTTAAACATACAGACCCCTGACCATTAATCTCCGGAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB GCCAATTCCTTCTTACCATCAAGAAAGACCTCCGGCTGTGTCATGCCCATGACATGC 440
QY 101 HisCysGlyGluGlnAlaMetLysLysTyrSerGlnIleLeuSerHisPheGlyLysLeu 120
DB CATTGTGGGAGAGAACATGAAGAAATACAGCCAAATCTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGlnAlaAlaValAlaLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
DB GAACCTCAGGCAAGCATTTGTGAAGGCTTTGGGGAACCTGACATTTCTTGCATAGATG 560
QY 141 GluGluThrGlu 144
DB 561 GAGAGACAGAA 572

RESULT 4

US-10-342-887-186
; Sequence 186, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernarde, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 186
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-186

Alignment Scores:
Pred. No.: 8.29e-93 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-789-129-26 (1-144) x US-10-342-887-186 (1-926)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgLysSer 20
DB 141 TGTGTGATCGCCACCAACCTTCAGAAATACGAAATGATTTTCTGACATACGGGCGAGT 200
QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40

DB 201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAACTTAAGAGAGACTGAGCTTTGCAA 260
QY 41 AspThrLysProAlaAsnArgCysCysGluLeuArgHisGluLeuArgLeuTyrLeuAsp 60
DB GACACAAAGCTCGCAATGATGATGCTGCTCCGCGCAATTTGCTAAGACTCTATCGGAC 320
QY 61 ArgValPheLysAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB AGGATTTTAAACATACAGACCCCTGACCATTAATCTCCGGAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB GCCAATTCCTTCTTACCATCAAGAAAGACCTCCGGCTGTGTCATGCCCATGACATGC 440
QY 101 HisCysGlyGluGlnAlaMetLysLysTyrSerGlnIleLeuSerHisPheGlyLysLeu 120
DB CATTGTGGGAGAGAACATGAAGAAATACAGCCAAATCTGAGTCACTTTGAAAAGCTG 500
QY 121 GluProGlnAlaAlaValAlaLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
DB GAACCTCAGGCAAGCATTTGTGAAGGCTTTGGGGAACCTGACATTTCTTGCATAGATG 560
QY 141 GluGluThrGlu 144
DB 561 GAGAGACAGAA 572

RESULT 5

US-10-789-129-1
; Sequence 1, Application US/10789129
; Publication No. US20040142428A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/789,129
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/413,661
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/199,586
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,597
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEPTIDE:
; NAME/KEY: CDS
; LOCATION: (45)...(572)
US-10-789-129-1

Alignment Scores:
Pred. No.: 8.29e-93 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-789-129-26 (1-144) x US-10-789-129-1 (1-926)

QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgLysSer 20
DB 141 TGTGTGATCGCCACCAACCTTCAGAAATACGAAATGATTTTCTGACATACGGGCGAGT 200
QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 201 GTGCAAGCCAAAGATGGAAACATTGACATCAGAAATCTTAAGAGAGACTGAGCTTTGCAA 260

```
QY 41 AspThrIlyProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCCTGCGAATGATGCTGCTCGCCATTGCTAAAGACTTATCTGGAGC 320
QY 61 ArgValPheIlyAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB 321 AGGGATTATTTAAACATACACGAGCCCTGACATTATACCTCCGGAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAATTCTCTTCTTACCATCAAGAAAGACCTCCGGCTGTGTCATGCCCACATGACATGC 440
QY 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
DB 441 CATTTGGGGAGAGCAATGAAATACAGCCAGATTGTAGTCACTTTGAAAGCTG 500
QY 121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
DB 501 GAACCTCAGGCACAGATTGTGAAGGCTTTGGGGAACTAGACATTTCTTGCAATGGATG 560
QY 141 GluGluThrGlu 144
DB 561 GAGGAGACAGAA 572

RESULT 6
US-10-789-251-1
; Sequence 1, Application US/10789251
; Publication No. US20040143097A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Haldeman, Betty A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/789,251
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/413,661
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/199,586
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,597
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(572)
US-10-789-251-1

Alignment Scores:
Pred. No.: 8,296-93 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-789-129-26 (1-144) x US-10-789-251-1 (1-926)
QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTGATCGCCAAACCTTCAGGAATACGAAATGGAATTTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 201 GTGCAGCCCAAGATGGAACATTTGACATCAGAACTTTAAGAGAGACTGAGTCTTGGCAA 260
QY 41 AspThrIlyProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCCTGCGAATGATGCTGCTCGCCATTGCTTAAGACTTATCTGGAGC 320
```

```
QY 61 ArgValPheIlyAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
DB 321 AGGGATTATTTAAACATACACGAGCCCTGACATTATACCTCCGGAAGATCAGACGCTC 380
QY 81 AlaAsnSerPheLeuThrIleLysLysAspLeuArgLeuCysHisAlaHisMetThrCys 100
DB 381 GCCAATTCTCTTCTTACCATCAAGAAAGACCTCCGGCTGTGTCATGCCCACATGACATGC 440
QY 101 HisCysGlyGluGluAlaMetLysLysTyrSerGlnIleLeuSerHisPheGluLysLeu 120
DB 441 CATTTGGGGAGAGCAATGAAATACAGCCAGATTCTGACATCTTGAAGAAAGCTG 500
QY 121 GluProGlnAlaAlaValValLysAlaLeuGlyGluLeuAspIleLeuLeuGlnTyrMet 140
DB 501 GAACCTCAGGCACAGATTGTGAAGGCTTTGGGGAACTAGACATTTCTTGCAATGGATG 560
QY 141 GluGluThrGlu 144
DB 561 GAGGAGACAGAA 572

RESULT 7
US-10-789-968-1
; Sequence 1, Application US/10789968
; Publication No. US20040152878A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Haldeman, Betty A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/789,968
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/413,661
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 09/199,586
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,597
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(572)
US-10-789-968-1

Alignment Scores:
Pred. No.: 8,296-93 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-789-129-26 (1-144) x US-10-789-968-1 (1-926)
QY 1 CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgGlySer 20
DB 141 TGTGTGATCGCCAAACCTTCAGGAATACGAAATGGAATTTCTGACATACGGGGCAGT 200
QY 21 ValGlnAlaLysAspGlyAsnIleAspIleArgIleLeuArgArgThrGlnSerLeuGln 40
DB 201 GTGCAGCCCAAGATGGAACATTTGACATCAGAACTTTAAGAGAGACTGAGTCTTGGCAA 260
QY 41 AspThrIlyProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyrLeuAsp 60
DB 261 GACACAAAGCCTGCGAATGATGCTGCTCGCCATTGCTTAAGACTTATCTGGAGC 320
QY 61 ArgValPheIlyAsnTyrGlnThrProAspHisTyrThrLeuArgLysIleSerSerLeu 80
```

Db 321 AGGATATTAAAACTACACAGACCCCTGACCTATATCTCCGGAAGATCAGACCCCTC 380
Qy 81 AAsenSerPheLeuThrIleYslyAspLeuArgLeuCyshiAlaHisMetThrCys 100
Db 381 GCCAATTCCTTTCTTACATCAAGAGAGACCTCCGGCTCTGTATGCCCAATGACATG 440
Qy 101 HISCYGLYGLUGLUALAWEtlySlyTYRserGlnIleuSerHisPheGluYsleu 120
Db 441 CATTGTGGGAGAGCAATGAAGAAATACAGCCCAATTCGTGATCACTTGGAAAAGCTG 500
Qy 121 GIUPROGlnAlaValValYslyAlaLeuGlygluLeuAspIleuLeuGlnTrpMet 140
Db 501 GAACCTCAGGACGAGCTGTGTGAAGCTTTGGGGAACTAGACATTCCTTGTGCAATGATG 560
Qy 141 GIUGluthrGlu 144
Db 561 GAGGAGACAGAA 572
RESULT 8
US-10-748-484-1
; Sequence 1, Application US/10748484
; Publication No. US20040181040A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Haldeman, Betty A.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE POLYPEPTIDE-10
; FILE REFERENCE: 97-72
; CURRENT APPLICATION NUMBER: US/10/748,484
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US/09/199,586
; PRIOR FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(572)
US-10-748-484-1
Alignment Scores:
Pred. No.: 8,296-93 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-789-129-26 (1-144) x US-10-748-484-1 (1-926)
Qy 1 CysValIleAlaThrAsnLeuGlnIuIleArgAnglyPheSerAspIleArgGlySer 20
Db 141 TGTGTGATCGCCACAACTTCAGGAATACGAATGATTTCTTGACATATAGGGGCACT 200
Qy 21 ValGlnAlaYsAspGlyAsnIleAspIleArgIleLeuArgArgThGlnSerLeuGln 40
Db 201 GTGCAAGCCAAAGATGAAACATTGACATCAANAATTAAAGAGAGACTGATGCTTTGCA 260
Qy 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisIleuLeuArgLeuTrpLeuAsp 60
Db 261 GACACAAAGCTTCGCAATCGATGCTGCTCTCGCCGCAATTCGTAAAGACTCTATCTGAGC 320
Qy 61 ArgValPheLysAsnTYRglnThrProAspHisTYRThrLeuArgLysIleSerSerLeu 80
Db 321 AGGATATTAAAACTACACAGACCCCTGACATTAATCTCCGGAAGATGAGAGCCCTC 380
Qy 81 AlaAsnSerPheLeuThrIleYslyAspLeuArgLeuCyshiAlaHisMetThrCys 100
Db 381 GCCAATTCCTTTCTTACATCAAGAGAGACCTCCGGCTCTGTATGCCCAATGACATGATGC 440

Qy 101 HISCYGLYGLUGLUALAWEtlySlyTYRserGlnIleuSerHisPheGluYsleu 120
Db 441 CATTGTGGGAGAGCAATGAAGAAATACAGCCCAATTCGTGATCACTTGAAGAAAGCTG 500
Qy 121 GIUPROGlnAlaValValYslyAlaLeuGlygluLeuAspIleuLeuGlnTrpMet 140
Db 501 GAACCTCAGGACGAGCTGTGTGAAGCTTTGGGGAACTAGACATTCCTTGTGCAATGATG 560
Qy 141 GIUGluthrGlu 144
Db 561 GAGGAGACAGAA 572
RESULT 9
US-10-994-116-1
; Sequence 1, Application US/10994116
; Publication No. US20050136004A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenteng
; APPLICANT: Kindvogel, Wayne
; APPLICANT: Chen, Zhi
; APPLICANT: Hughes, Steven D.
; APPLICANT: Chandrasekhar, Yaemin A.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Lehnert, Joyce M.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Sivakumar, Pallavar V.
; TITLE OF INVENTION: ANTI-IL-20 ANTIBODIES AND BINDING PARTNERS AND METHODS OF USING
; FILE REFERENCE: 03-21
; CURRENT APPLICATION NUMBER: US/10/994,116
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: US 60/524,131
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/555,857
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)...(575)
US-10-994-116-1
Alignment Scores:
Pred. No.: 8,296-93 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-789-129-26 (1-144) x US-10-994-116-1 (1-926)
Qy 1 CysValIleAlaThrAsnLeuGlnIuIleArgAnglyPheSerAspIleArgGlySer 20
Db 141 TGTGTGATCGCCACAACTTCAGGAATACGAATGATTTCTTGACATATAGGGGCACT 200
Qy 21 ValGlnAlaYsAspGlyAsnIleAspIleArgIleLeuArgArgThGlnSerLeuGln 40
Db 201 GTGCAAGCCAAAGATGAAACATTGACATCAANAATTAAAGAGAGACTGATGCTTTGCA 260
Qy 41 AspThrLysProAlaAsnArgCysCysLeuLeuArgHisIleuLeuArgLeuTrpLeuAsp 60
Db 261 GACACAAAGCTTCGCAATCGATGCTGCTCTCGCCGCAATTCGTAAAGACTCTATCTGAGC 320
Qy 61 ArgValPheLysAsnTYRglnThrProAspHisTYRThrLeuArgLysIleSerSerLeu 80
Db 321 AGGATATTAAAACTACACAGACCCCTGACATTAATCTCCGGAAGATGAGAGCCCTC 380

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QY 81 aaasrserpheuutrllelyslasphleuaygleuQyHiaHahisectThryS 100
Db 381 GCCAAATTCCTTTCTTACCATCAAGAGACCTCGGGCTCTGTCAATGCCACATGACATGC 440
QY 101 HieCyGglYgluJua1aMeLylbYrYserGln1leLeuSerXishpGluYslau 120
Db 441 CATTGTGGGAGAGAAAGCATTAAGAAATACAGCCAGATTCTAGTACCTTTGAAAAGCTG 500
QY 121 GluPrGln1a1a1aVal1yAla1eug1YgluLeuAp1leLeuLeuGlnTpmet 140
Db 501 GAACCTCAGCAGCAGCTGTGAAGGCTTTGGGGGAACTAGACATTCCTTGCAATGATG 560
QY 141 GluGluThrGlu 144
Db 561 GAGGAGACAGAA 572

RESULT 10
US-10-994-151-1
; Sequence 1, Application US/10994151
; Publication NO. US20050170468A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; APPLICANT: Hughes, Steven D.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Lehner, Joyce M.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Sivakumar, Pallavur V.
; APPLICANT: Moore, Margaret D.
; TITLE OF INVENTION: ANTI-IL-20 RECEPTOR ANTIBODIES AND BINDING PARTNERS AND METHODS
; FILE REFERENCE: IN INFLAMMATION
; CURRENT APPLICATION NUMBER: US/10/994,151
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: US 60/524,131
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/555,857
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45) ... (575)
US-10-994-151-1

Alignment Scores:
Pred. No.: 8,29e-93 Length: 926
Score: 753.00 Matches: 144
Percent Similarity: 100.00% Conservatvie: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-789-129-26 (1-144) x US-10-994-151-1 (1-926)
QY 1 CyeVal1le1a1atrAsn1leuGln1u1leArGaenGlyPheseraAp1leArGlySer 20
Db 141 TGTGTGATCGCCACAAACCTTCAGGAATACAAATGATTTCTGACATACGGGCGACT 200
QY 21 ValGln1a1yAspGlyAsn1leAp1leArG1leLeuArG1rThrg1uSerLeuGln 40
Db 201 GTGCAACCAAAAGATGCAAACTTGACATCAGAACTTAAAGAGACCTGAGTCTTGCAA 260
QY 41 AspThryrPco1aaasrArGyCySleuLeuArGHiSleuLeuArGleuYr1leuAsp 60
Db 261 GACACAAAGCCTGGGAATCGATGCTGCTCCCTGCGCGCATTTGGTAAGACTTATCTTGAC 320

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| | | | |
|--|-----|--|-----|
| QY | 6 | ArgValPheIysAsnIstYrGlnThrProAspHisYrTrpLeuAqIyIsIeSerSetLeu | 80 |
| Db | 321 | AGGATATTAAACCTACCAAGACCCCTGACCATTTACTCTCCGGAAGATACGAGCTC | 368 |
| QY | 81 | AlaAsnSerPheLeuThrIleIyIsIyAspLeuAqIeUyShIsaIhiImetThrCys | 100 |
| Db | 381 | GCCAATTCCTTTCTTACGATCAAGAAGACCTCCGGCTCTGTACATGCCACATGACATGC | 440 |
| QY | 101 | HisCyGlyGluGluAlaMetIyIsIyTrsGlnIleLeuSerHisPheGluIyLeu | 120 |
| Db | 441 | CATTGTGGGAGGAGAACCAATGAAAGAAATACACCCGATTCGAGTCACATTTTGAAGACCTG | 500 |
| QY | 121 | GluProGlnAlaIleValIyIsAlaLeuGlyIleuAspIleLeuLeuGlnTrpMet | 140 |
| Db | 501 | GAACCTCAGGACCACTTGTGAAGGCTTTGGGGGAACCTAGACATTTCTTCTGCAATGGAATG | 560 |
| QY | 141 | GluGluThrGlu | 144 |
| Db | 561 | GAGGAGACAGAA | 572 |
| RESULT 11 | | | |
| US-10-122-882B-14 | | | |
| ; Sequence 14, Application US/10122882B | | | |
| ; Publication No. US20030228657A1 | | | |
| GENERAL INFORMATION: | | | |
| ; APPLICANT: POMDER, TRACEY | | | |
| ; APPLICANT: CHAN, CHUNG | | | |
| ; TITLE OF INVENTION: METHODS FOR ENHANCING THE TRANSLATION | | | |
| ; TITLE OF INVENTION: AND EXPRESSION OF RECOMBINANT PROTEINS | | | |
| ; FILE REFERENCE: 01-15 | | | |
| ; CURRENT APPLICATION NUMBER: US/10/122,882B | | | |
| ; CURRENT FILING DATE: 2002-04-12 | | | |
| ; PRIOR APPLICATION NUMBER: 60/283,668 | | | |
| ; PRIOR FILING DATE: 2001-04-13 | | | |
| ; NUMBER OF SEQ ID NOS: 25 | | | |
| ; SOFTWARE: FastSeq for Windows Version 4.0 | | | |
| ; SEQ ID NO 14 | | | |
| ; LENGTH: 462 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Homo sapiens | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: misc feature | | | |
| ; LOCATION: 10... (0) | | | |
| ; OTHER INFORMATION: codon optimized for E. coli | | | |
| US-10-122-882B-14 | | | |
| Alignment Scores: | | | |
| Pred. No.: 1,01e-92 Length: 462 | | | |
| Score: 749.00 Matches: 143 | | | |
| Percent Similarity: 100.00% Conservative: 1 | | | |
| Best Local Similarity: 99.31% Mismatches: 0 | | | |
| Query Match: 99.47% Indels: 0 | | | |
| DB: 6 Gaps: 0 | | | |
| US-10-769-129-26 (1-144) x US-10-122-882B-14 (1-462) | | | |
| QY | 1 | CysValIleAlaThrAsnLeuGlnGluIleArgAsnGlyPheSerAspIleArgIySer | 20 |
| Db | 28 | TGTGTGATCGCCACCAACCTGCGAGAAATCCGTAAAGGTTTCTCGAGATCCGTGGCGGC | 87 |
| QY | 21 | ValGlnAlaIyAspGlyAsnIleAspIleArgIleIleuAqArgTrpGluSerLeuGln | 40 |
| Db | 88 | GTCGAGGCGCAAAATAGTAACATGTGACATCCGTATCCGTGCGTGAACCGAGTCTTGGAG | 144 |
| QY | 41 | AspThrIySerProAlaAsnArgCysCybLeuLeuArgHisLeuLeuArgLeuTyTrpLeuAsp | 60 |
| Db | 148 | GACACCAAAACCGCGGAACCGTTGCTGCTGCTGCGCCGCACTGCTGCTGATCTGGAC | 207 |
| QY | 61 | ArgValPheIyAsnIyTrpGlnThrProAspHisYrTrpLeuAqIyIsIeSerSetLeu | 80 |
| Db | 208 | CGTGTCTTTCAAAAATCAACGAGACCCGGACCACTATACCTGCGCTAAATACAGCAGCCTG | 267 |
| QY | 81 | AlaAsnSerPheLeuThrIleIyIsIyAspLeuAqIeUyShIsaIhiImetThrCys | 100 |

Db 268 GCCAACTCCTCTTGACCAATCAAAAAAGACCTGCTGTGTCACCCCACTGACCTGC 327
Qy 101 HtSGYGLYGLUGLALAMETLYSLYSTRSERGHLLEUSERHSHPHEGLUYLSLEU 120
Db 328 CACTGTGTGAGGAGAACCAATGAAAAATACGCCAATTCGTGACCACTTCGAAAAACTG 387
Qy 121 GIUPROGINALALAVALLYSALALEUGLYGLULEUASPILLEULEUGINTPMEC 140
Db 388 GAACCGGAGGAGCACTGTGTGAAGCTCTGGTGAACCTGCACTTCTGTCAGTGGATG 447
Qy 141 GIUGLUTHGLU 144
Db 448 GAGAGAGCCGAA 459

RESULT 12

US-11-054-063-18
; Sequence 18, Application US/11054063
; Publication No. US20050164349A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Powder, Tracey
; TITLE OF INVENTION: METHODS FOR ENHANCING EXPRESSION OF
; FILE OF INVENTION: RECOMBINANT PROTEINS
; FILE REFERENCE: 03-22C1
; CURRENT APPLICATION NUMBER: US/11/054,063
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 11/008,853
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/529,412
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-054-063-18

Alignment Scores:

Pred. No.: 1,01e-92 Length: 462
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
Gaps: 0

US-10-789-129-26 (1-144) x US-11-054-063-18 (1-462)

Qy 1 CysVal11leAlaThAsnLeuGlnGluIleArgAngLYPheSerAsp11leArgLYSer 20
Db 28 TGTGATGTCGACCACTGACGAAATCCGTAACGGTTCTCTGAGATCCGTGACAC 87
Qy 21 ValGlnAlaLYAspG1YAsn11leAsp11leArg11leuArgArgThrg1uSerLeuGln 40
Db 88 GTGACGGCCAAAGATGTAACTGATGACATCCGTATCTGCGTACGATCCGATCTGACG 147
Qy 41 AspThrySProAlaAsnArgCYsCYleuLeuArgH1sleuLeuArgLeuTYrLeuAsp 60
Db 148 GACACCAAAACCGGCAACCGTTGCGCTGCGCCGACCTGCTCGTGTATCTGAGC 207
Qy 61 ArgVal1PheLYAsnTYrGlnThrProAspH1sTYrThrLeuArgLYleSerSerLeu 80
Db 208 CGTGTTCCTTCAAAAATACCAAGACCCCGACCACTTACCTCGTAAATTCAGACGCTG 267
Qy 81 AlaAsnSerPheLeuThr11eLYsLYsAspLeuArgLeuCYsH1sAlaH1sMetThrCYs 100
Db 268 GCCAACTCCTTCTGACCATCAAAAAGACCTGCTGTGTGCAAGCCCACTGACCTGCG 327
Qy 101 HtSGYGLYGLUGLALAMETLYSLYSTRSERGHLLEUSERHSHPHEGLUYLSLEU 120
Db 328 CACTGTGTGAGGAGAACCAATGAAAAATACGCCAATTCGTGACCACTTCGAAAAACTG 387

Qy 121 GIUPROGINALALAVALLYSALALEUGLYGLULEUASPILLEULEUGINTPMEC 140
Db 388 GAACCGGAGGAGCACTGTGTGAAGCTCTGGTGAACCTGCACTTCTGTCAGTGGATG 447
Qy 141 GIUGLUTHGLU 144
Db 448 GAGAGAGCCGAA 459

RESULT 13

US-10-122-882B-17
; Sequence 17, Application US/10122882B
; Publication No. US20030228657A1
; GENERAL INFORMATION:
; APPLICANT: POMDER, TRACEY
; APPLICANT: CHAN, CHUNG
; TITLE OF INVENTION: METHODS FOR ENHANCING THE TRANSLATION
; FILE OF INVENTION: AND EXPRESSION OF RECOMBINANT PROTEINS
; FILE REFERENCE: 01-15
; CURRENT APPLICATION NUMBER: US/10/122,882B
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/283,668
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of EC and SEQ ID NO:14, codon optimized for
US-10-122-882B-17

Alignment Scores:

Pred. No.: 1.19e-92 Length: 513
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
Gaps: 0

US-10-789-129-26 (1-144) x US-10-122-882B-17 (1-513)

Qy 1 CysVal11leAlaThAsnLeuGlnGluIleArgAngLYPheSerAsp11leArgLYSer 20
Db 139 GTGACGGCCAAAGATGTAACTGATGACATCCGTATCTGCGTACGATCCGATCTGACG 198
Qy 41 AspThrySProAlaAsnArgCYsCYleuLeuArgH1sleuLeuArgLeuTYrLeuAsp 60
Db 199 GACACCAAAACCGGCAACCGTTGCTGCTGCGCCGACCTGCTCGTGTATCTGAGC 258
Qy 61 ArgVal1PheLYAsnTYrGlnThrProAspH1sTYrThrLeuArgLYleSerSerLeu 80
Db 259 CGTGTTCCTTCAAAAATACCAAGACCCCGACCACTTACCTCGTAAATTCAGACGCTG 318
Qy 81 AlaAsnSerPheLeuThr11eLYsLYsAspLeuArgLeuCYsH1sAlaH1sMetThrCYs 100
Db 319 GCCAACTCCTTCTGACCATCAAAAAGACCTGCTGTGTGCAAGCCCACTGACCTGCG 378
Qy 101 HtSGYGLYGLUGLALAMETLYSLYSTRSERGHLLEUSERHSHPHEGLUYLSLEU 120
Db 379 CACTGTGTGAGGAGAACCAATGAAAAATACGCCAATTCGTGACCACTTCGAAAAACTG 438
Qy 121 GIUPROGINALALAVALLYSALALEUGLYGLULEUASPILLEULEUGINTPMEC 140
Db 439 GAACCGGAGGAGCACTGTGTGAAGCTCTGGTGAACCTGCACTTCTGTCAGTGGATG 498
Qy 141 GIUGLUTHGLU 144

Db 499 GAGGAGACCGAA 510

RESULT 14
US-10-467-431-1
; Sequence 1, Application US/10467431
; Publication No. US20040092445A1
; GENERAL INFORMATION:
; APPLICANT: Hewer, Josef
; APPLICANT: Liu, Ling
; APPLICANT: Timothy, Noblitt
; TITLE OF INVENTION: USE OF LP82 TO TREAT HEMATOPOIETIC DISORDERS
; FILE REFERENCE: X-14753
; CURRENT APPLICATION NUMBER: US/10/467,431
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: 60/272,242
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/332,740
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (272)..(799)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (272)..(325)
; OTHER INFORMATION:
US-10-467-431-1

Alignment Scores:
Pred. No.: 2,666-92 Length: 867
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
DB: 7 Gaps: 0

US-10-789-129-26 (1-144) x US-10-467-431-1 (1-867)

QY 1 CysvalilleaIaThrAenLeuGIngiIeaRgaenGlyPheSeraspIleaRgiYser 20
Db 368 TGTGTGATCGCCCAAACTTCAGAAATGGAATGATTTCTGAGATACGGGGCAGT 427
QY 21 ValGlnAlaIyAspGlyAsnIleaRpiIleaRgiIleuAArgThrgIuseRleuGln 40
Db 428 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGAGAGACTGAGTCTTGCAA 487
QY 41 AspThrLyProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyRleuAap 60
Db 488 GACACAAAGCCCTGCGAATGATGCTGCTCTGCGCATTTGCTAAGACTCTATCTGAGC 547
QY 61 ArgValPheLyAsnTyRgInThrProAspHisTyRThrLeuArgIyIleSerSerLeu 80
Db 548 AGGATATTAAAACTACAGAGACCCCTGACCATTAATCTCTCGGAAAGATCACAGGCTC 607
QY 81 AlaAsnSerPheLeuThrIleTyRlyAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db 608 GCCAATTCCTTTCTTACATCAAGAAAGACCTCGGCTCTGTCAATGCCCATGACATGAC 667
QY 101 HisCysGlyGluGluAlaMetCysTyRSerGlnIleLeuSerHisPheGluTyRLeu 120
Db 668 CATTGTGGGAGAGAGCAATGAAAGAAATACAGCCAGATTTCTGAGTCACTTGAAAAGCTG 727
QY 121 GluProGlnAlaAlaValIyAlaIyAlaLeuGlyGluLeuAapIleLeuLeuGlnTrpMet 140
Db 728 GAACCTCAGGCAAGAGATTGTGAAGGCTTTGGGGGAACTAGACATTTCTTGCATATGATG 787
QY 141 GluGluThrGlu 144

Db 788 GAGGAGACAGAA 799

RESULT 15
US-10-466-695A-1
; Sequence 1, Application US/1046695A
; Publication No. US20040162237A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Nyles W
; TITLE OF INVENTION: USE OF LP82 TO TREAT BODY WEIGHT DISORDERS
; FILE REFERENCE: X-14544
; CURRENT APPLICATION NUMBER: US/10/466,695A
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: 60/264,239
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (272)..(799)
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (272)..(325)
US-10-466-695A-1

Alignment Scores:
Pred. No.: 2,666-92 Length: 867
Score: 749.00 Matches: 143
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.31% Mismatches: 0
Query Match: 99.47% Indels: 0
DB: 7 Gaps: 0

US-10-789-129-26 (1-144) x US-10-466-695A-1 (1-867)

QY 1 CysvalilleaIaThrAenLeuGIngiIeaRgaenGlyPheSeraspIleaRgiYser 20
Db 368 TGTGTGATCGCCCAAACTTCAGAAATGGAATGATTTCTGAGATACGGGGCAGT 427
QY 21 ValGlnAlaIyAspGlyAsnIleaRpiIleaRgiIleuAArgThrgIuseRleuGln 40
Db 428 GTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGAGAGACTGAGTCTTGCAA 487
QY 41 AspThrLyProAlaAsnArgCysCysLeuLeuArgHisLeuLeuArgLeuTyRleuAap 60
Db 488 GACACAAAGCCCTGCGAATGATGCTGCTCTGCGCATTTGCTAAGACTCTATCTGAGC 547
QY 61 ArgValPheLyAsnTyRgInThrProAspHisTyRThrLeuArgIyIleSerSerLeu 80
Db 548 AGGATATTAAAACTACAGAGACCCCTGACCATTAATCTCTCGGAAAGATCACAGGCTC 607
QY 81 AlaAsnSerPheLeuThrIleTyRlyAspLeuArgLeuCysHisAlaHisMetThrCys 100
Db 608 GCCAATTCCTTTCTTACATCAAGAAAGACCTCGGCTCTGTCAATGCCCATGACATGAC 667
QY 101 HisCysGlyGluGluAlaMetCysTyRSerGlnIleLeuSerHisPheGluTyRLeu 120
Db 668 CATTGTGGGAGAGAGCAATGAAAGAAATACAGCCAGATTTCTGAGTCACTTGAAAAGCTG 727
QY 121 GluProGlnAlaAlaValIyAlaIyAlaLeuGlyGluLeuAapIleLeuLeuGlnTrpMet 140
Db 728 GAACCTCAGGCAAGAGATTGTGAAGGCTTTGGGGGAACTAGACATTTCTTGCATATGATG 787
QY 141 GluGluThrGlu 144

Job time : 823 secs

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